

Fig. 1

Mutant-specific oligonucleotide primers used for mutant number 1. Mutated nucleotide underlined.

<i>Bet v 1</i> sense	5' - AATTATGAGACT <u>GAGACCAC</u> CTCTGTTATCCCAGCAGCTCG	-3'
<i>Bet v 1</i> non-sense	3' - TTAATACTCTGACTCT <u>GGTGG</u> GACAATAGGGTCGTCGAGC	-5'
sense primer	5' - TGAGACC <u>CC</u> CTCTGTTATCCCAG	-3'
non-sense primer	3' - ATACTCTGACTCT <u>GGGGG</u> GACA	-5'

J. M. S. J. R. S. J. M. S. J. R. S.

Fig. 2

Oligonucleotide primers for site directed mutagenesis of
Bet v 1 (No. 2801).

all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4: 186Bv, 31-mer 5'-GATAACCCTCTTCCACAGGTTGCACCCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATGCCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTTCCTGAAATGTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTCCCGAA
4	non-sense	9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCACATGCAAACCTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTTCCTCAGGCCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTCAATGTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCACTGGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

Fig. 3**Overview of all Bet v 1 mutations**

1 (A-C)											
G	G	T	G	T	T	A	T	T	G	A	G
V	V	F	N	Y	E	T	E	T	T-P	S	V
60											
I	P	A	A	R	L	F	K				
20											
9 (A-G) 2 (A-C) 2 (A-C)											
G	C	C	T	T	T	A	T	G	G	C	A
C	C	T	T	G	A	T	G	G	C	A	T
T	T	T	A	T	C	C	T	T	C	C	A
T	T	T	G	A	G	G	T	G	A	C	T
A	A	G	G	A	C	C	T	T	C	C	G
A	G	A	G	A	C	C	T	T	C	C	T
120											
A	F	I	L	D-G	G	D	N-T	L	F	P	K-Q
F	I	L	D	G	G	D	N	T	L	P	K-Q
P	K	A	P	Q	V	A	P	Q	A	I	S
K	A	P	Q	V	A	P	Q	A	I	S	S
40											
3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 (GA-TC)											
G	T	T	G	A	A	G	A	A	G	A	G
T	T	G	A	A	G	A	A	G	A	G	T
T	G	A	A	G	A	A	G	A	A	G	T
G	A	A	G	A	A	G	A	A	G	T	C
A	G	A	A	G	A	A	G	A	A	G	T
A	G	A	A	G	A	A	G	A	A	G	T
180											
V	E	N	I	E-S	G	N-S	G	G	P	G	T
E	N	I	E-S	G	N-S	G	G	P	G	T	I
S	G	N	S	G	G	P	G	T	I	K	K-N
G	N	S	G	G	P	G	T	I	K	K-N	I
P	G	T	I	K	K-N	I	S	F	P	E-S	S
G	T	I	K	K-N	I	S	F	P	E-S	S	S
60											
5 (CA-TG)											
G	G	C	T	C	T	T	C	A	G	T	G
G	C	T	C	T	T	C	A	G	T	G	T
C	T	C	T	T	C	A	G	T	G	T	G
C	T	C	T	T	C	A	G	T	G	T	G
T	A	C	T	T	C	A	G	T	G	T	G
A	T	C	T	T	C	A	G	T	G	T	G
A	T	C	T	T	C	A	G	T	G	T	G
240											
G	L	P	F	K	Y	V	K	D	R	V	D
L	P	F	K	Y	V	K	D	R	V	D	E
P	F	K	Y	V	K	D	R	V	D	E	V
F	K	Y	V	K	D	R	V	D	H	T-A	N
K	Y	V	K	D	R	V	D	H	T-A	N	F
Y	V	K	D	R	V	D	H	T-A	N	F	K
80											
TACAATTACAGCGTGATCGAGGGCGGTCCCATAGCGACACATTGGAGAAGATCTCAAAC											
T	A	C	A	T	T	C	A	T	G	A	G
A	T	T	C	A	T	G	A	G	A	G	T
A	T	T	C	A	T	G	A	G	A	G	T
T	A	C	A	T	T	C	A	T	G	A	G
A	T	T	C	A	T	G	A	G	A	G	T
300											
Y	N	Y	S	V	I	E	G	G	P	I	G
N	Y	S	V	I	E	G	G	P	I	G	D
Y	S	V	I	E	G	G	P	I	G	D	T
S	V	I	E	G	G	P	I	G	D	T	L
V	I	E	G	G	P	I	G	D	T	L	E
I	E	G	G	P	I	G	D	T	L	E	K
E	G	G	P	I	G	D	T	L	E	K	I
G	G	P	I	G	D	T	L	E	K	I	S
100											
10 (GAG-CAC) 8 (CCC-TGG)											
G	A	G	A	G	A	T	G	G	A	G	T
A	T	G	A	T	G	G	A	G	A	G	T
A	T	G	A	T	G	G	A	G	A	G	T
T	G	A	T	G	A	T	G	G	A	G	T
G	A	T	G	A	T	G	G	A	G	A	T
A	T	G	A	T	G	G	A	G	A	G	T
360											
E	I	K	I	V	A	T	P-G	D	G	G	S
I	K	I	V	A	T	P-G	D	G	G	S	I
K	I	V	A	T	P-G	D	G	G	S	I	L
I	V	A	T	P-G	D	G	G	S	I	L	K
V	A	T	P-G	D	G	G	S	I	L	K	I
A	T	P-G	D	G	G	S	I	L	K	I	S
T	P-G	D	G	G	S	I	L	K	I	S	N
P-G	D	G	G	S	I	L	K	I	S	N	K
D	G	G	S	I	L	K	I	S	N	K	Y
G	G	S	I	L	K	I	S	N	K	Y	
120											
CACACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTAAAGCAAGTAAAGAAATGGGC											
H	T	K	G	D	H	E	V	K	A	E	Q
T	K	G	D	H	E	V	K	A	E	Q	V
K	G	D	H	E	V	K	A	E	Q	V	K
G	D	H	E	V	K	A	E	Q	V	K	A
D	H	E	V	K	A	E	Q	V	K	A	E
H	E	V	K	A	E	Q	V	K	A	E	M
E	V	K	A	E	Q	V	K	A	E	M	G
V	K	A	E	Q	V	K	A	E	M	G	
K	A	E	Q	V	K	A	E	M	G		
A	E	Q	V	K	A	E	M	G			
E	Q	V	K	A	E	M	G				
Q	V	K	A	E	M	G					
V	K	A	E	M	G						
K	A	E	M	G							
A	E	M	G								
E	M	G									
M	G										
G											
420											
H											
T											
L											
R											
A											
V											
E											
S											
Y											
L											
A											
H											
S											
D											
A											
Y											
N											
stop											
480											
GAGACACTTTGAGGGCCGTTGAGAGCTACCTCTGGCACACTCCGATGCCCTACAACAA											
TAA											
E											
T											
L											
R											
A											
V											
E											
S											
Y											

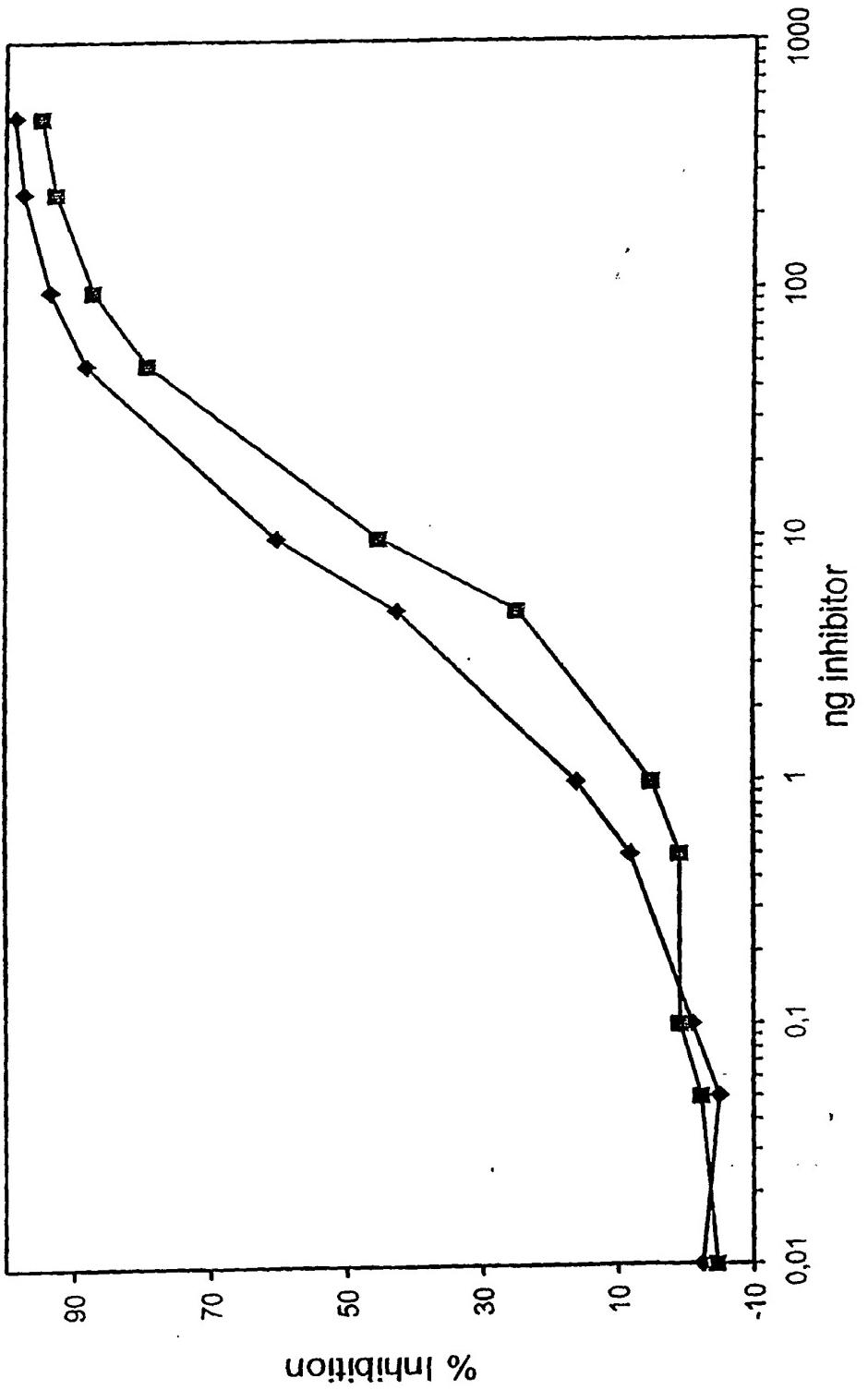


Fig. 4 → Bet v 1 → Glu45Ser

Yield %

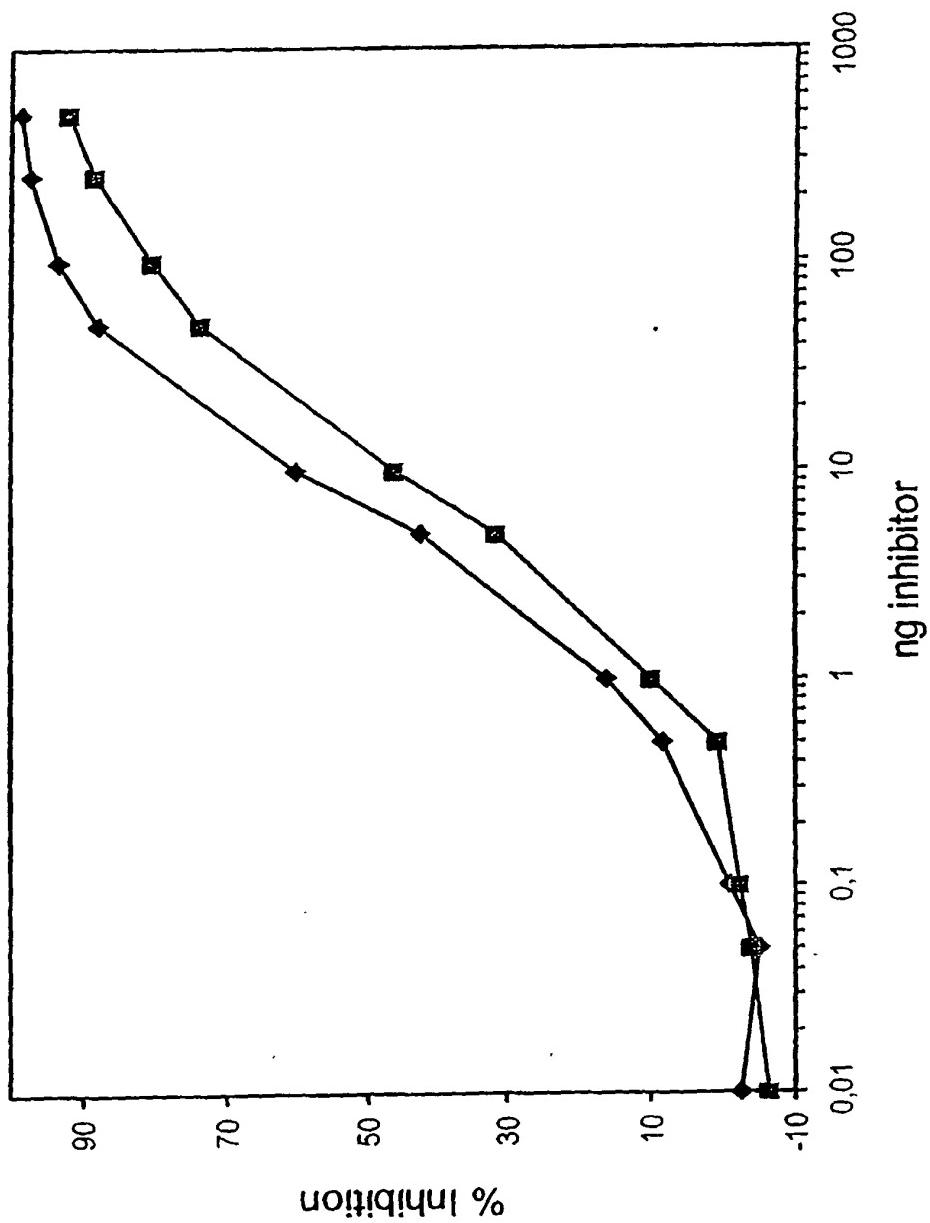
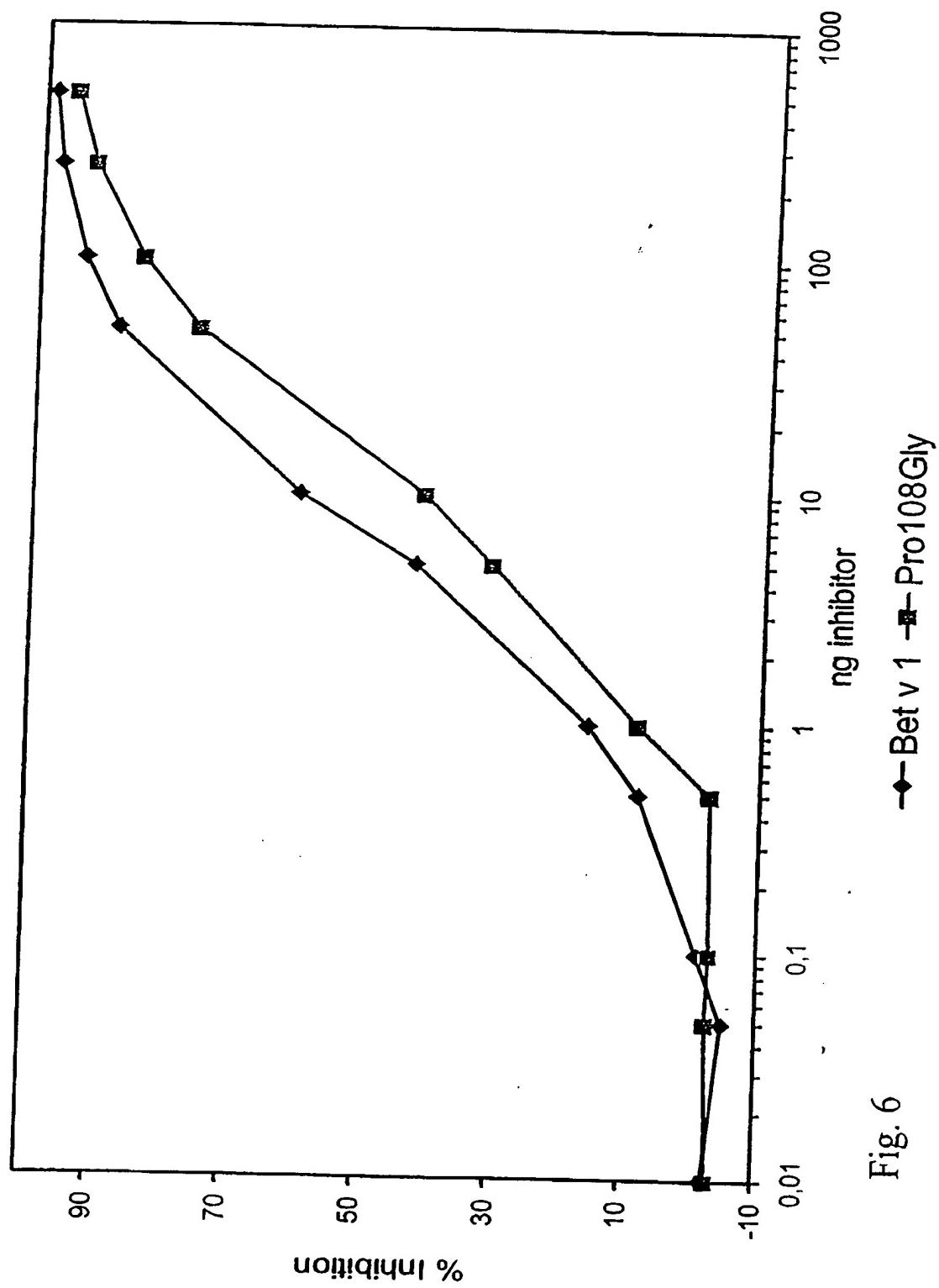


Fig. 5 —♦— Bet v 1 —■— Asn28Thr+Lys32Gln



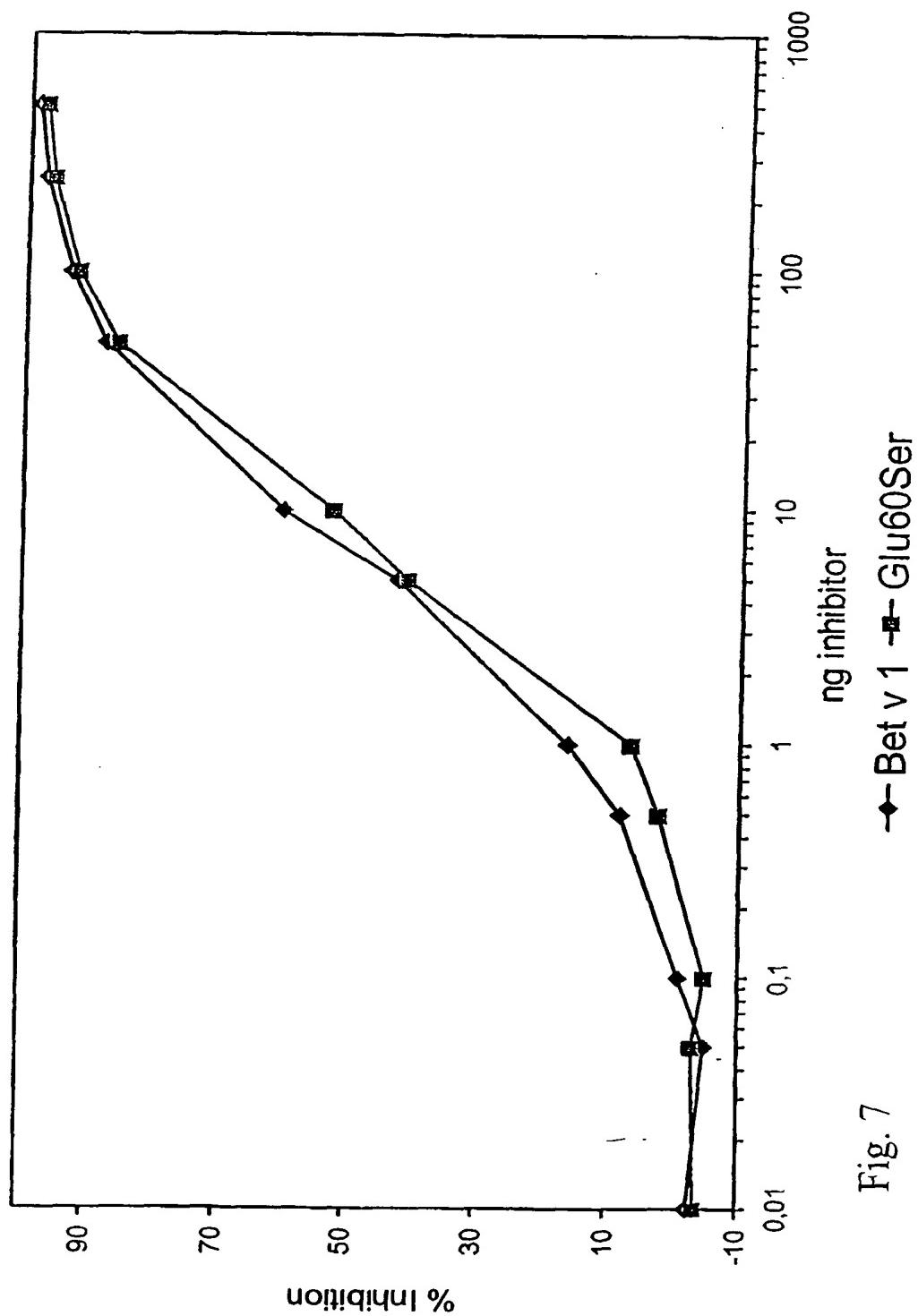


Fig. 7

→ Bet v 1 → Glu60Ser

10mM Na₂HPO₄/NaH₂PO₄ 0.025M NaCl

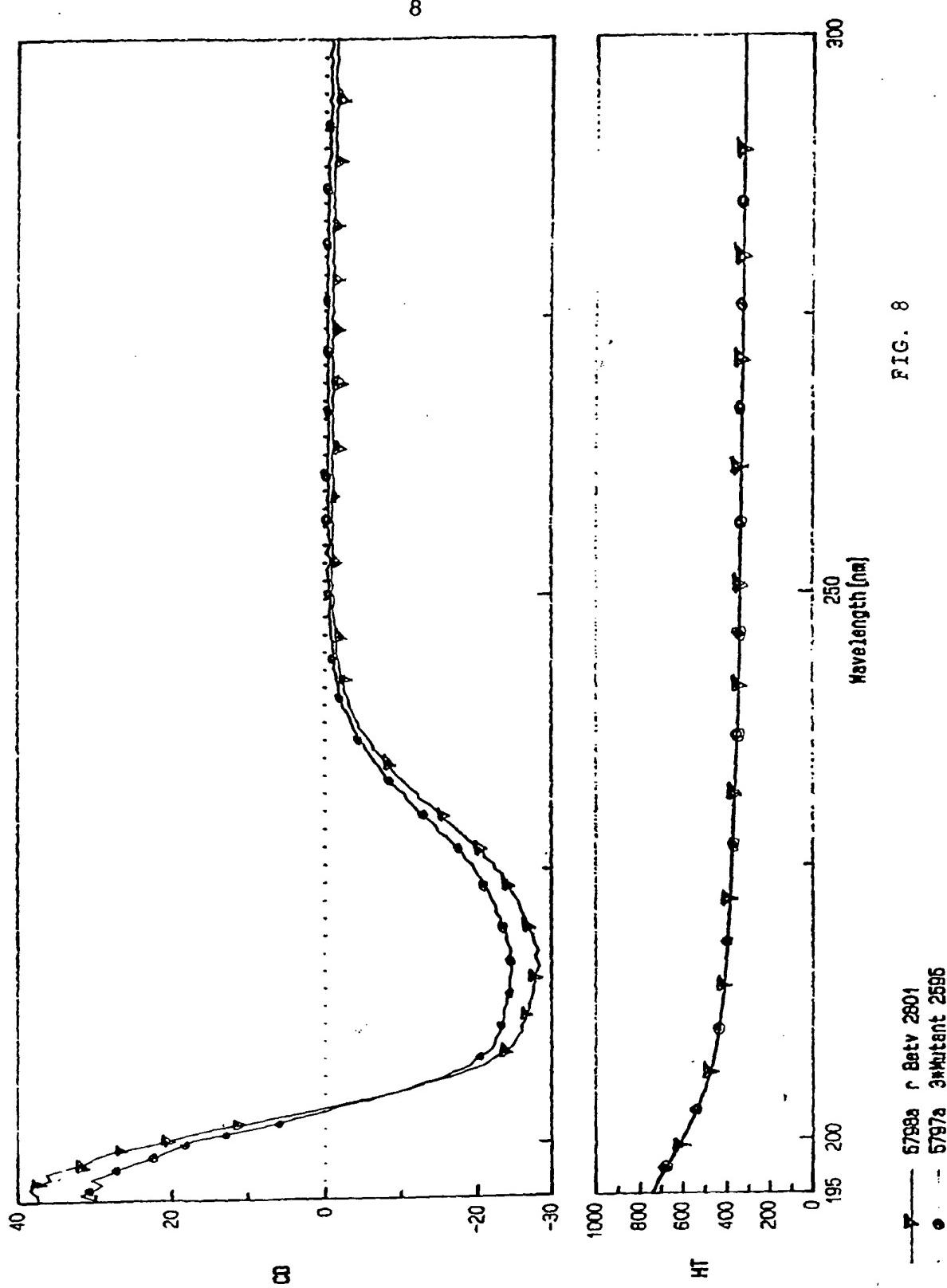
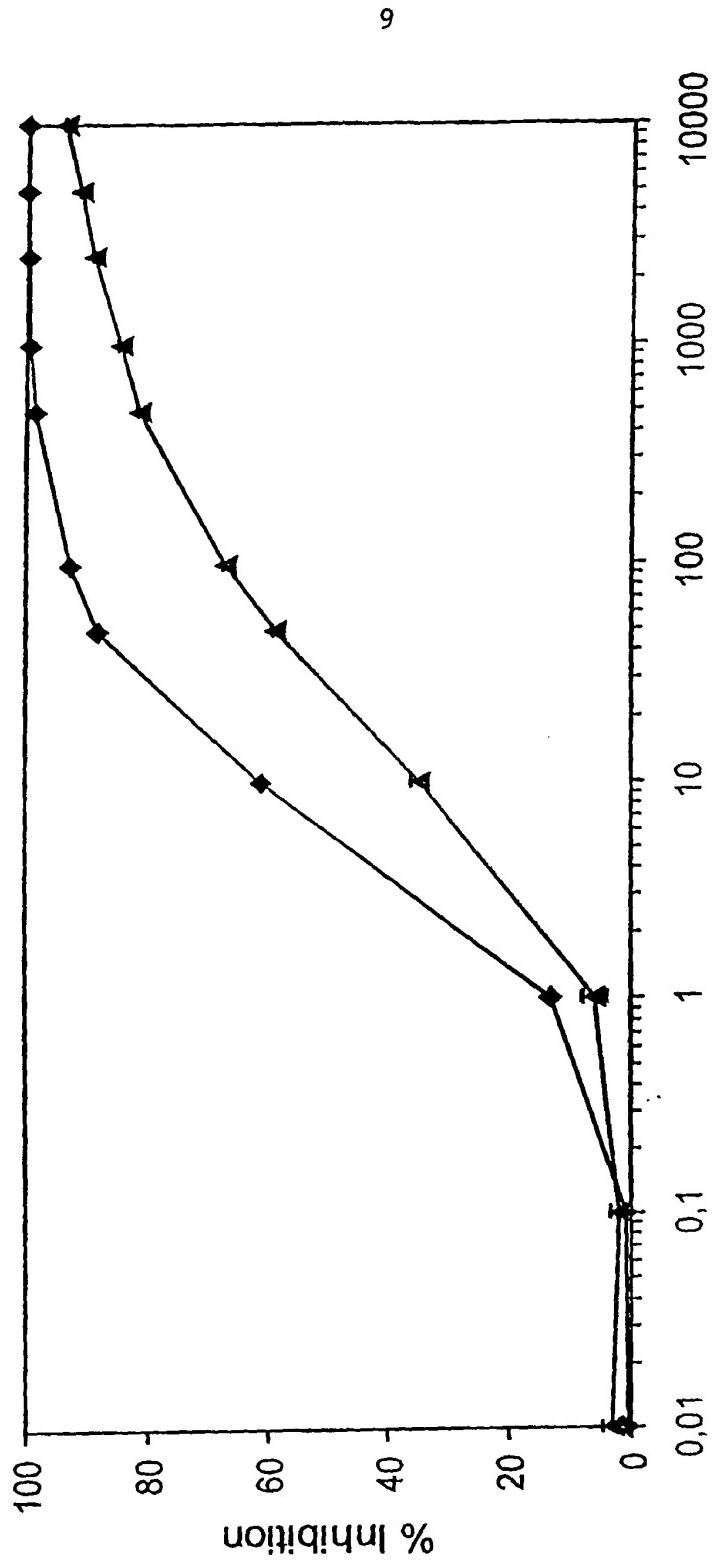


FIG. 8

Fig. 9

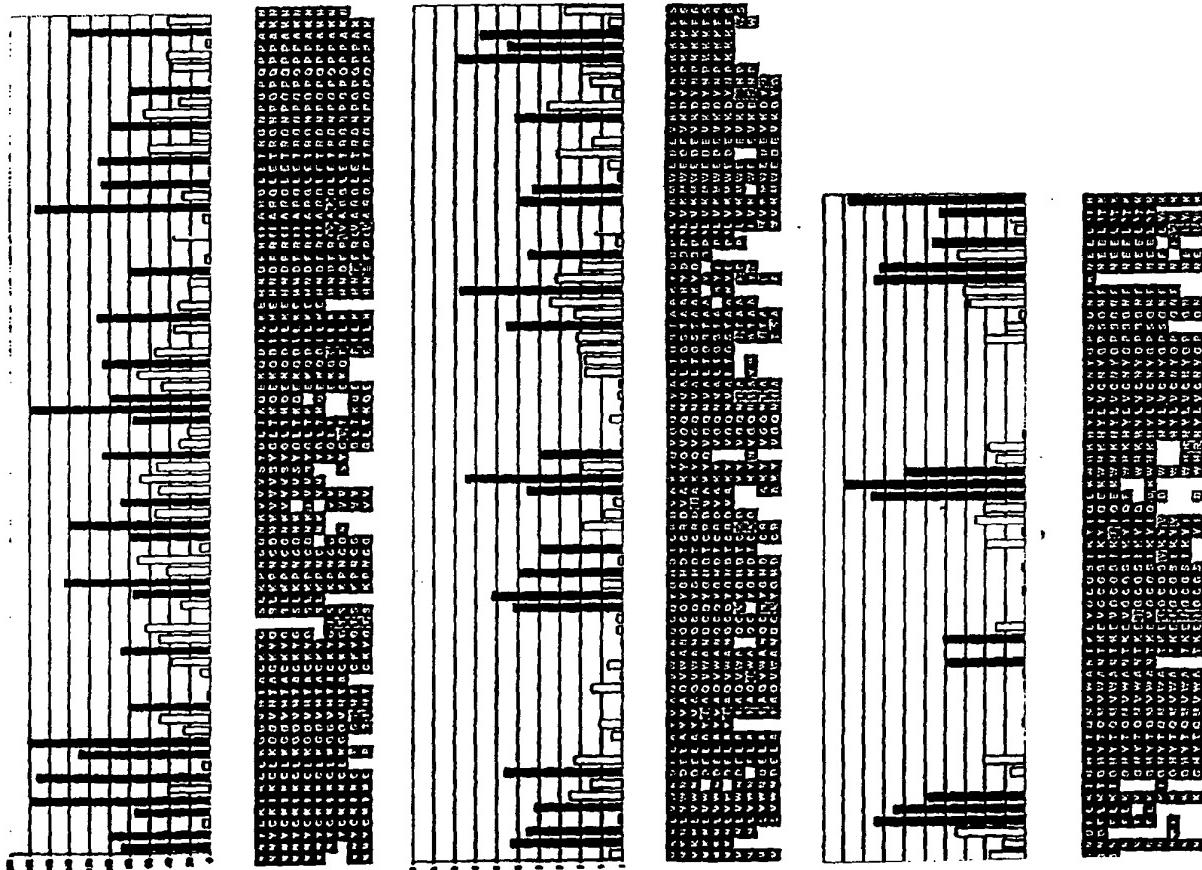
—♦— Bet v 1 —★— Glu45Ser, Pro108Gly, Asn28Thr+Lys32Gln.

ng inhibitor



Y Q S F Y T V R D E T P A G T

Conserved residues among Vespuila antigen 5



10

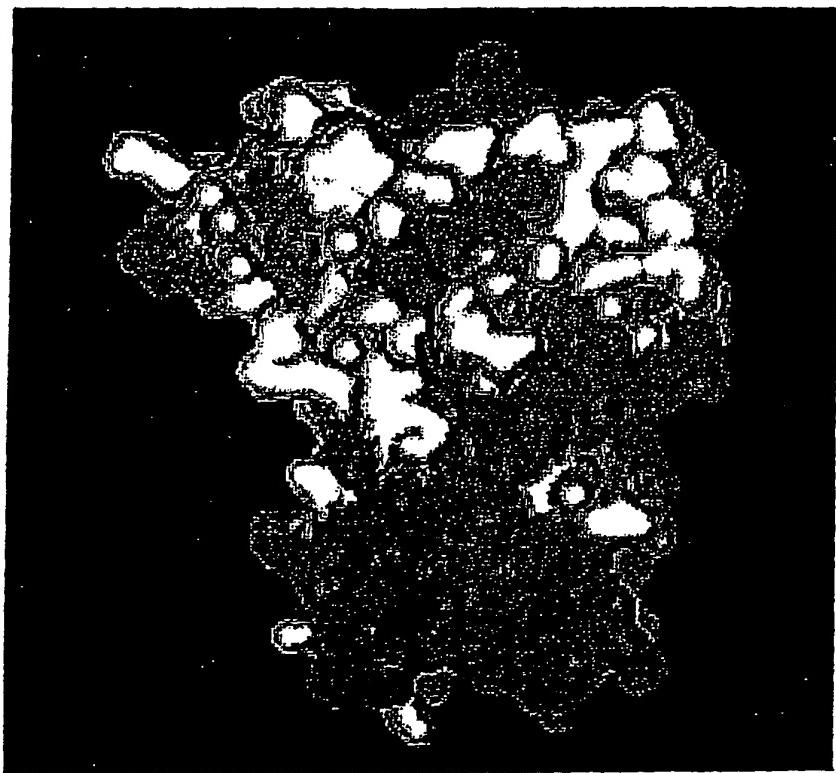


Figure 10.

Fig.11

Mutant-specific oligonucleotide primers used for Ves v 5 mutants.
Mutated nucleotides underlined.

Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5'- ACCACAGCCTCCAGCGAAGAATATGAAAAATTGGTATGGA	-3'
Ves v 5 non-sense	3'- TGGTGTCGGAGGTGCGTTCTTATACTTTAAACCATAACCT	-5'
sense primer	5'- CC <u>AGCGG</u> CTAATATGAAAAAT	-3'
non-sense primer	3'- GTCGGAGGTG <u>CGCC</u> GATTATAAC	-5'

Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5'- GGCTAACATGTCAATATGGTCACGATACTTGCAGGGATG	-3'
Ves v 5 non-sense	3'- CCGATTAGTTACAGTTACCCAGTGCTATGAACGTCCCTAC	-5'
sense primer	5'- TGTCA <u>AAG</u> CTGGTCACGATACT	-3'
non-sense primer	3'- TTAGTTACAGTT <u>CG</u> ACCAGTG	-5'

Fig. 12

12

Oligonucleotide primers for site directed mutagenesis of Ves v 5.

all sense 1: XhoI start, 38-mer:

EcoRI
5'-CCGCTCGAGAAAAGAAACATTATTGTAAAAATAAAATG
L E K R N N Y C K I K
Kex2 cleavage site amino terminus of Ves v 5

1	sense	1: K72As	21-mer	5'-CCAGCGGCTAATATGAAAAAT
1	non-sense	2: K72Aa	21-mer	5'-CATATTAGCCGCTGGAGGCTG
2	sense	3: Y96As	21-mer	5'-TGTCAAGCTGGTCACGATACT
2	non-sense	4: Y96Aa	21-mer	5'-GTGACCAGCTTGACATTGATT
				,
	all non-sense	7: CT-pPICZαA,	21-mer	5'-ATTCAATCAGCTGCGAGATAGG

Fig. 13

13

Overview of Ves v 5 mutations

1	AACAATTATTGTAAAATAAAATGTTGAAAGGAGGTGTCCATACTGCC	TGCAAATATGGA	60
1	N N Y C K I K C L K G G V H T A C K Y G		20
61	AGTCTAAACCGAATTGCGGTAATAAGTAGTGGTATCCTATGGTCTAAC	GAAACAAGAG	120
21	S L K P N C G N K V V V S Y G L T K Q E		40
121	AAACAAGACATCTTAAAGGAGCACAATGACTTTAGACAAAAAATTG	CACGAGGATTGGAG	180
41	K Q D I L K E H N D F R Q K I A R G L E		60
1 [K72A] (AAG-GCT)			
181	ACTAGAGGTAATCCTGGACCACAGCCTCCAGCG <u>A</u> GAATATGAAAATTGGTATGGAAC		240
61	T R G N P G P Q P P A K N M K N L V W N		80
2 [Y96A] (TA-GC)			
241	GACGAGTTAGCTTATGTCGCCAAGTGTGGCTAACATGTCAATATGGTCACGATACT		300
81	D E L A Y V A Q V W A N Q C Q Y G H D T		100
301	TGCAGGGATGTAGCAAAATATCAGGTTGGACAAACGTAGCCTAACAGGTAGCACGGCT		360
101	C R D V A K Y Q V G Q N V A L T G S T A		120
361	GCTAAATACGATGATCCAGTTAAACTAGTTAAATGTGGGAAGATGAAGTGAAAGATTAT		420
121	A K Y D D P V K L V K M W E D E V K D Y		140
421	AATCCTAACGAAAAAGTTTGGGAAACGACTTTCTGAAAACCGGCCATTACACTCAAATG		480
141	N P K K K F S G N D F L K T G H Y T Q M		160
481	GTTTGGGCTAACACCAAGGAAGTTGGTGTGGAAAGTATAAAATACATTCAAGAGAAATGG		540
161	V W A N T K E V G C G S I K Y I Q E K W		180
541	CACAAACATTACCTTGTATGTAATTATGGACCCAGCGGAAACTTTAAGAATGAGGAAC	TT	600
181	H K H Y L V C N Y G P S G N F K N E E L		200
601	TATCAAACAAAGTAA		612
201	Y Q T K stop		204

N O O D E - D A Y E D P

Yves v 5 Lys72Ala Tyr96Ala

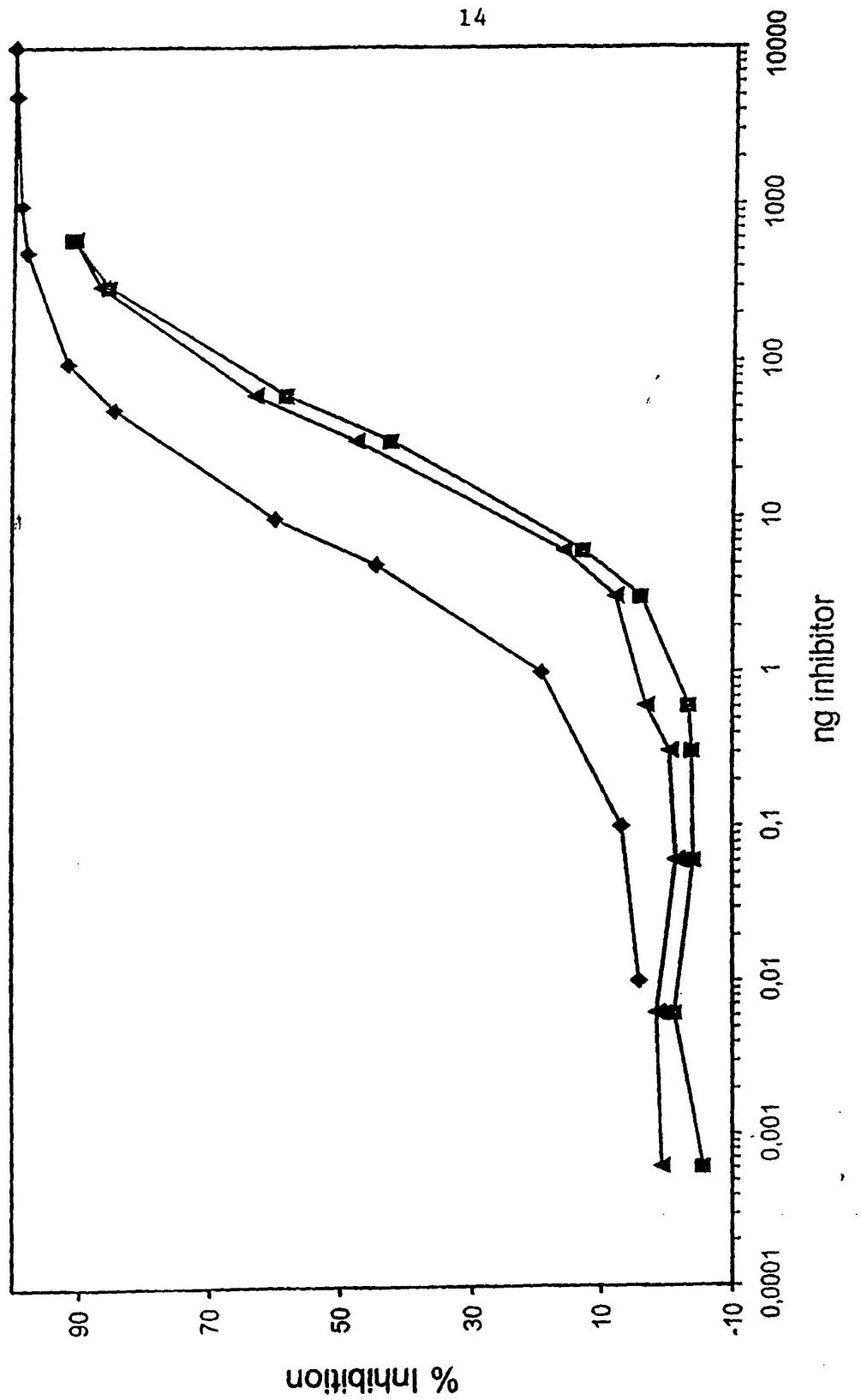
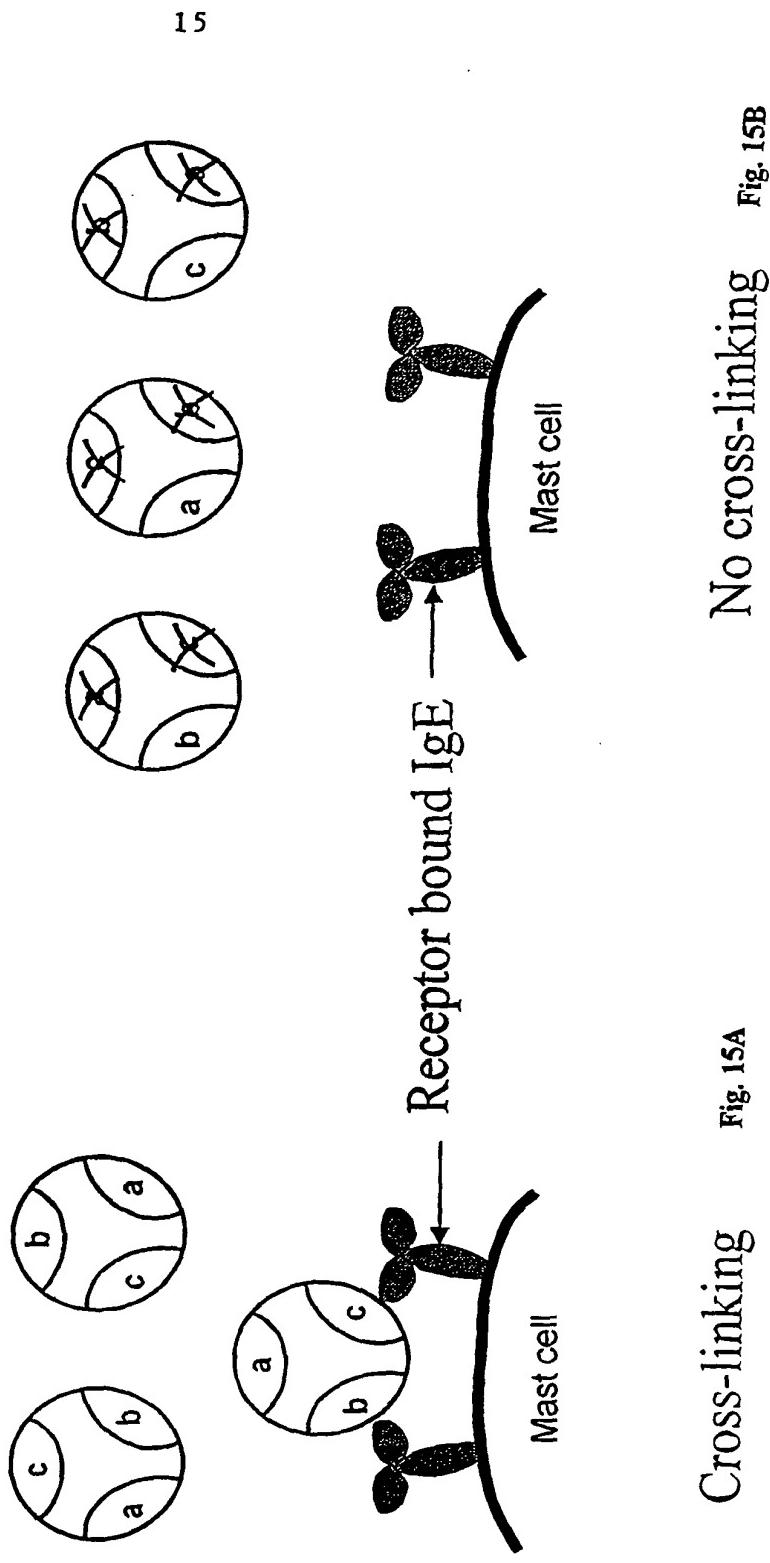


Fig. 14

◆—rYves v 5 ■—Lys72Ala ★—Tyr96Ala

Fig. 15

Effect of point mutations in dominating IgE epitopes
hypothetical model with 3 epitopes



Cross-linking

Fig. 15A

No cross-linking

Fig. 15B

Fig. 16**DNA SEQUENCE**

Der p 2 (DNA sequence referred to in notes in accession No. P49278 SWISSPROT)

ORIGIN

```

1      cacaattct tcttttttcc ttactactga tcattaatct gaaaaacaaaa ccaaacaaaac
61     cattcaaaat gatgtacaaa atttgtgtc tttcaitgtt ggtgcagcc gttgcctgt
121    atcaagtgcg tgcacaagat tggccaaatc atgaaaatcaa aaaagtttg gtaccaggat
181    gccatggtc agaaccatgt atcattcatc gtggtaaacc attccaattt gaagccgtt
241    tcgaagccaa cccaaacaca aaaacggcta aaattgaaat caaagcctca atcgatgg
301    tagaaggta tggtcccggt atcgatccaa atgcattgcata ttacatgaaa tgcccatgg
361    ttaaaggaca acaaatatgt attaaatata catggaatgt tccgaaaatt gcaccaaaat
421    ctgaaaatgt tgcgtcact gttaaagtta tgggtgtatga tgggttttg gcctgtgct
481    ttgctactca tgctaaaatc cgcgataaa tcaaaacaaaa ttattgtatt ttgtaatcac
541    aaatgttgc ttttttcc aaaaaaaaaa taaaataaaat ttggaaatt c

```

AMINO ACID SEQUENCE

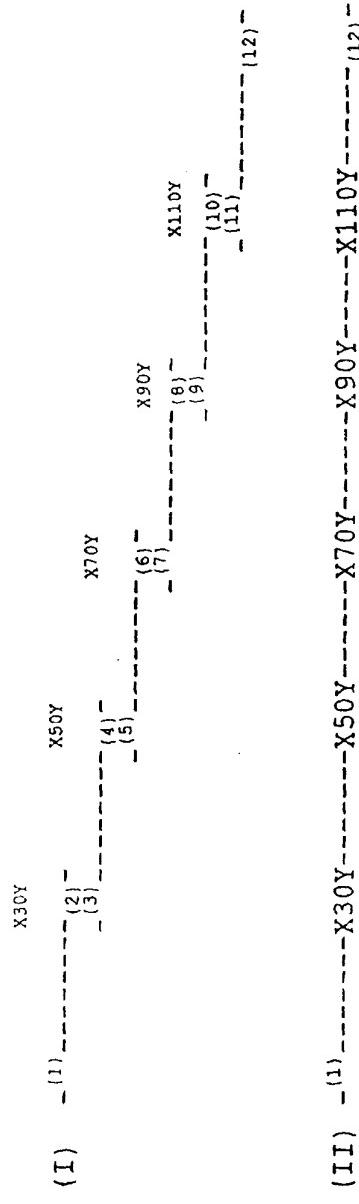
Der p 2 (Accession No. P49278 SWISSPROT; includes signal peptide 1-17)

```

1      mmykilclsl lvaavardqv dvkdcanhei kkvlvpgch sepciihrgk pfqleavfea
61     nqntktakie ikasidglev dvggidpnac hymkcplvkg qqydikytwn vpkiaksen
121    vvvtkvmgd dgvlacaiat hakird

```

Figure 17



Lines represents DNA sequences.

Numbers in parentheses above lines represents sense oligonucleotide primers: (1), (3), (5), (7), (9), (11).
Numbers in parentheses below lines represents anti-sense oligonucleotide primers: (2), (4), (6), (8), (10), (12).
Notation X (position) Y represents mutations.

- (1) Represents the sense oligonucleotide primer accommodating the protein N-terminus.
(12) Represents the anti-sense oligonucleotide primer accommodating the protein C-terminus.

Figure 18

Bet v 1 (2628) (Y5V, E45S, K65N, K97S, K134E)

DNA template: Bei v 1 (2589) carrying the Y5Y mutation.

Bet v 1 (2637)

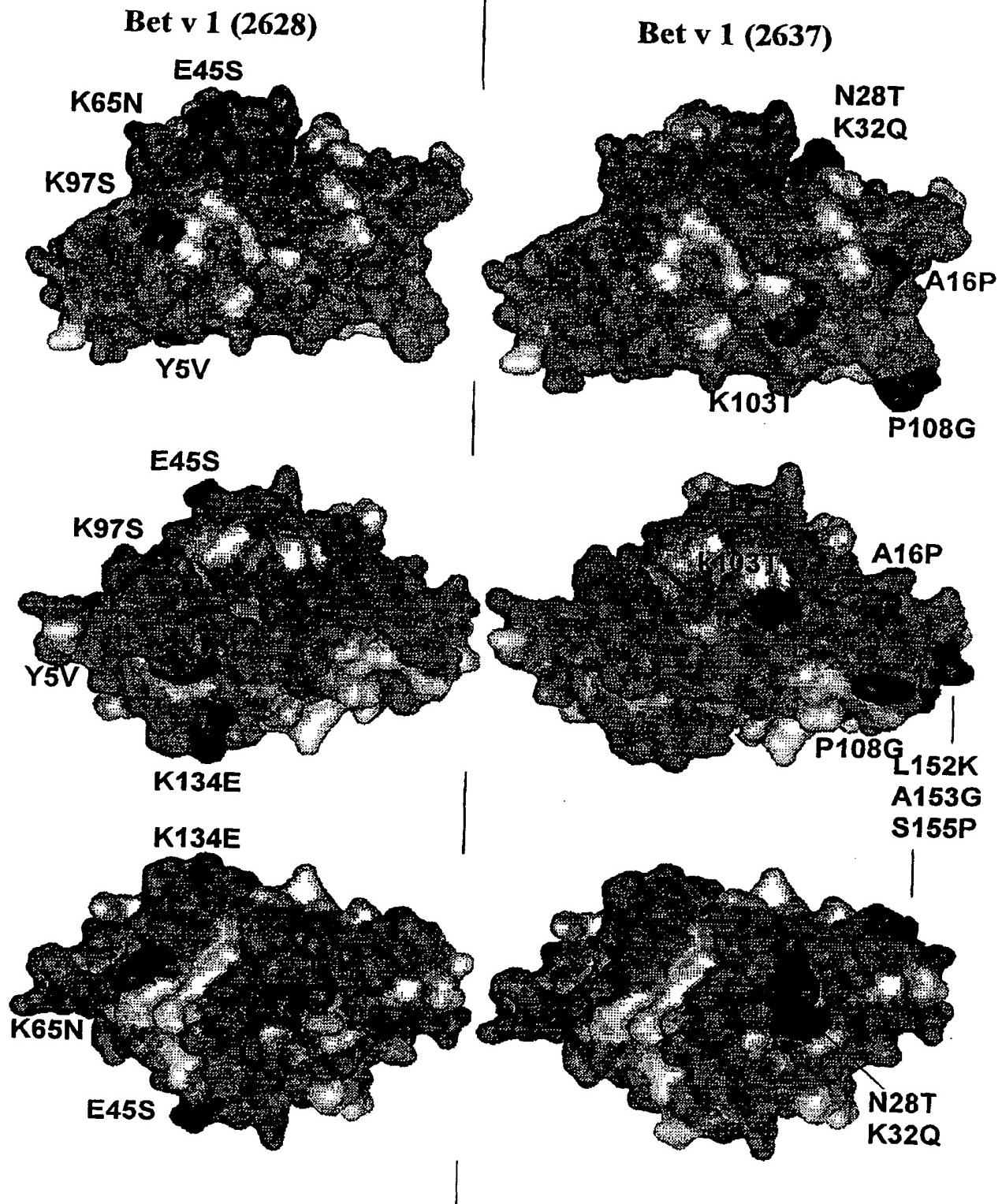
(A16P, N28T, K32Q, K103T, P108G, L152K, A153G, S155P)

DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations.

3331 Ma/c (s)

331 n Male

100031245 - 332504



Molecular surface of Bet v 1.

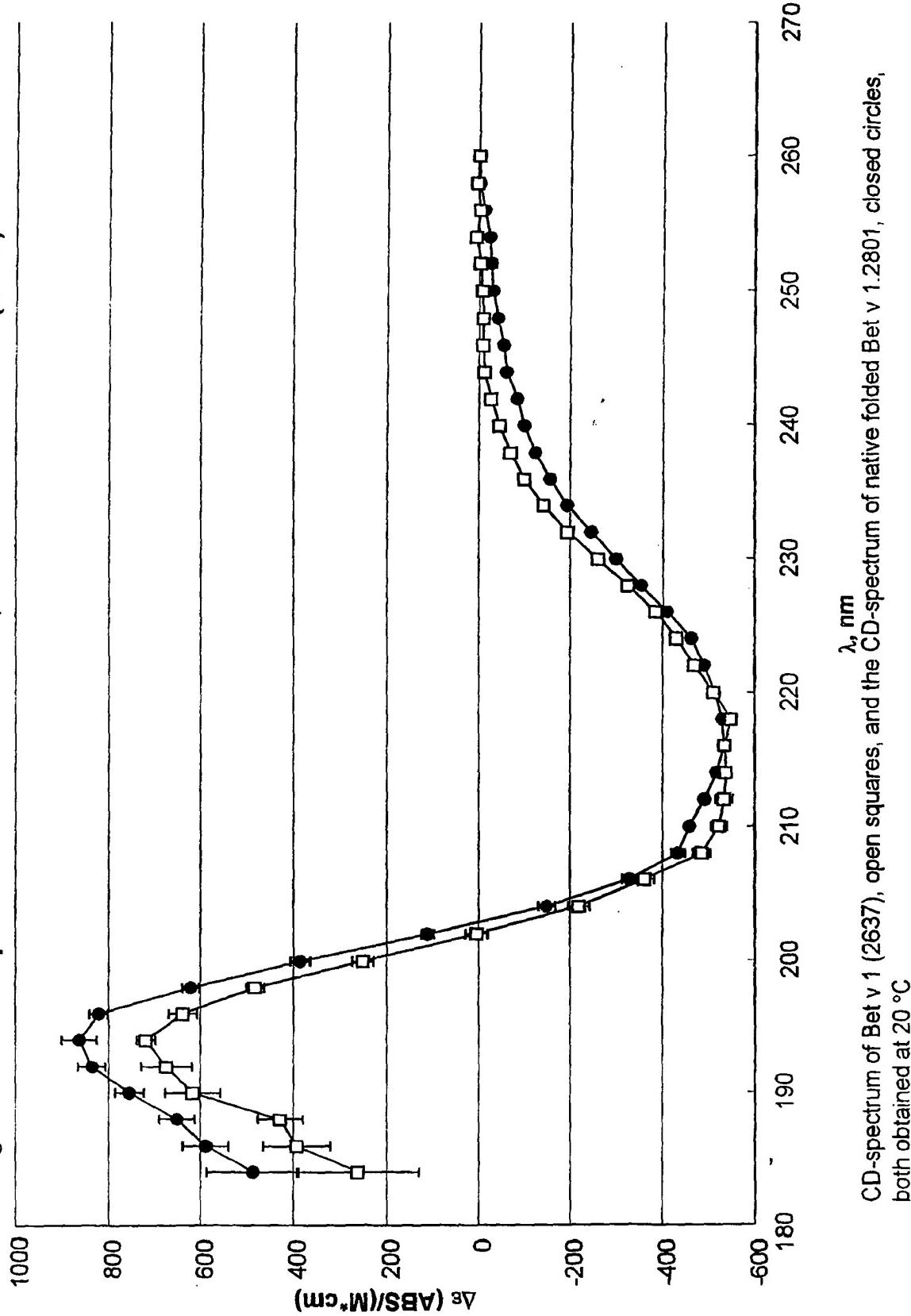
Left side: Bet v 1 (2628), Right side: Bet v 1 (2637)

Grey: Backbone + amino acids 95-100% conserved among *Fagales*

Black: Introduced point mutations.

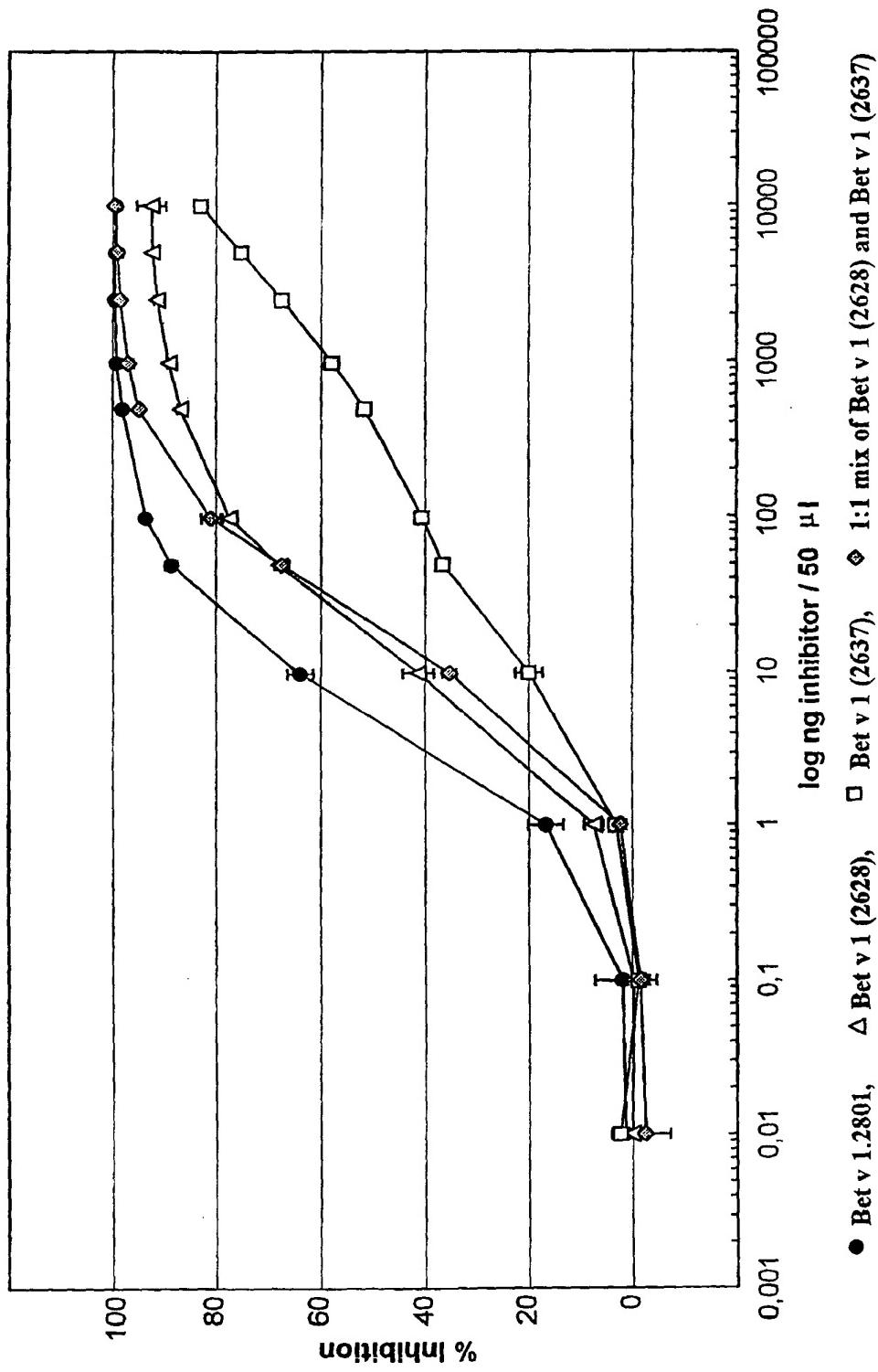
Figure 19

Figure 20 CD-spectrum of Bet v 1.2801, and mutant Bet v 1 (2637)



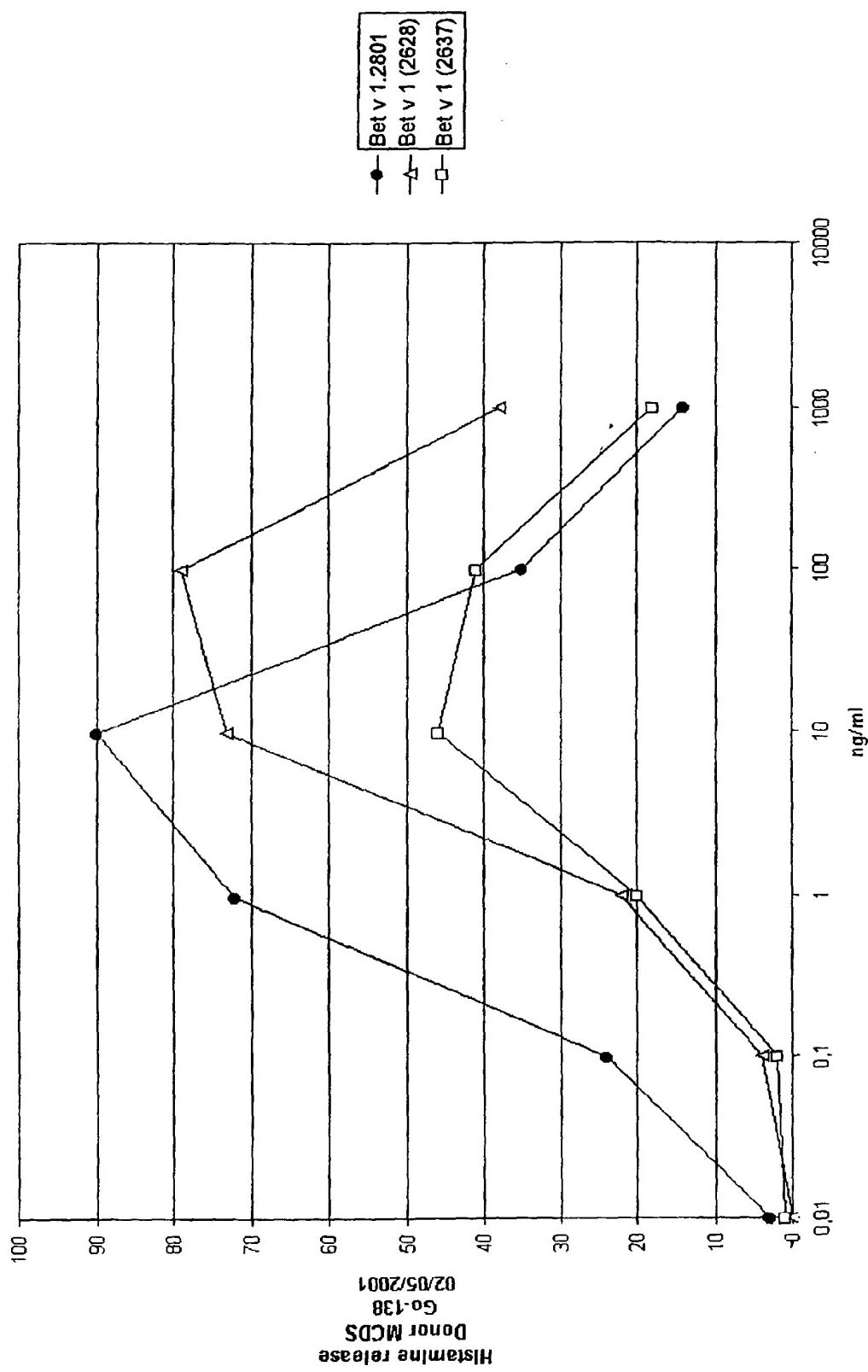
Y O S T T T T T T T T T T T T T T T T

Figure 21
Inhibition of human serum IgE-binding to Bet v 1.2801
with Bet v 1.2801 and mutated Bet v 1 allergens



Y 3 T Y = T T T T

Figure 22 Histamine release, donor MCDS, Bet v 1.2801, Bet v 1(2628), Bet v 1 (2637)



Y: 35 30 25 20 15 10 5 0
X: 10000 1000 100 10 1 0,1

Figure 23 Histamine release, donor MDH, Bet v 1.2801, Bet v 1(2628), Bet v 1 (2637)

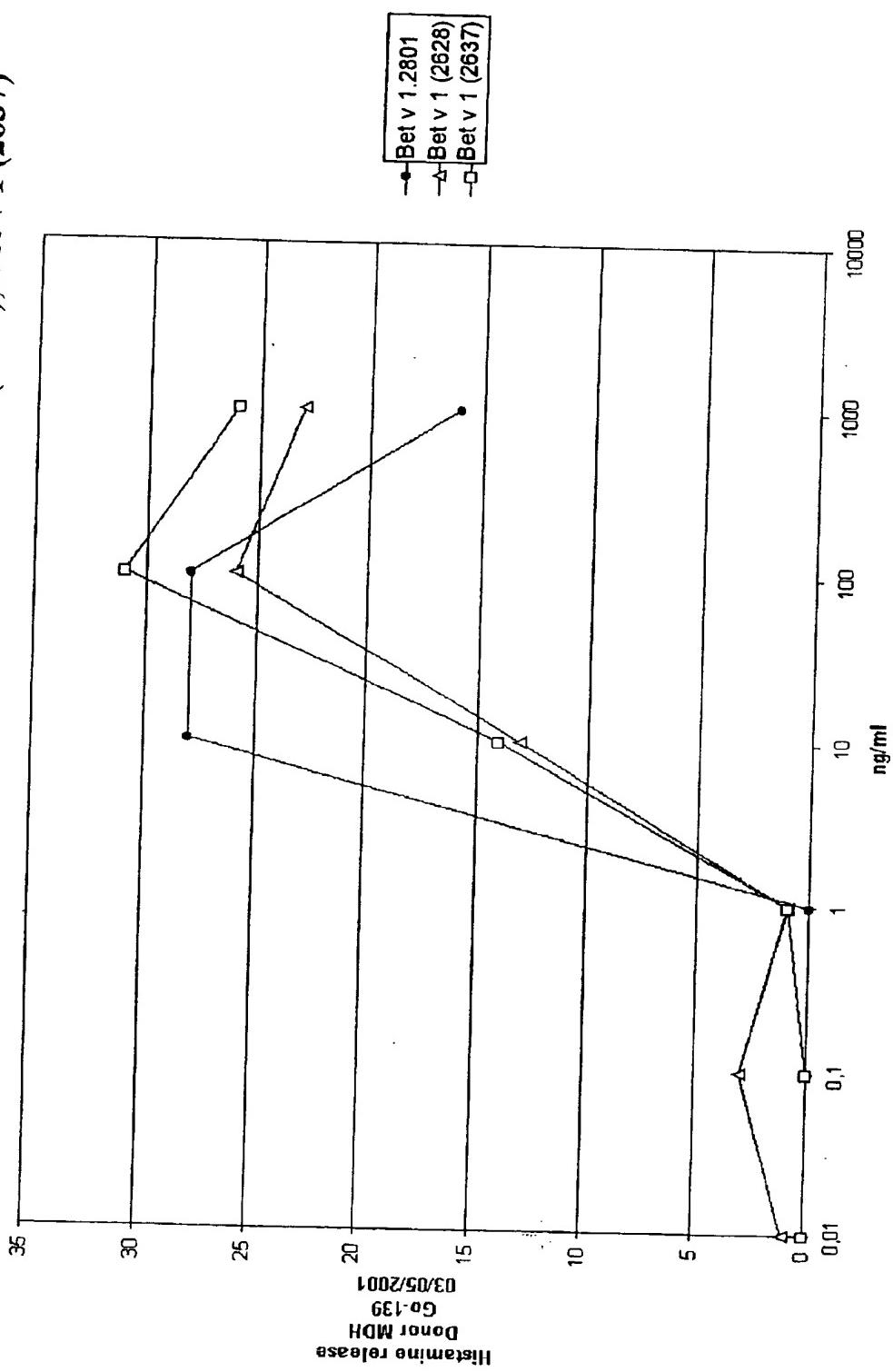
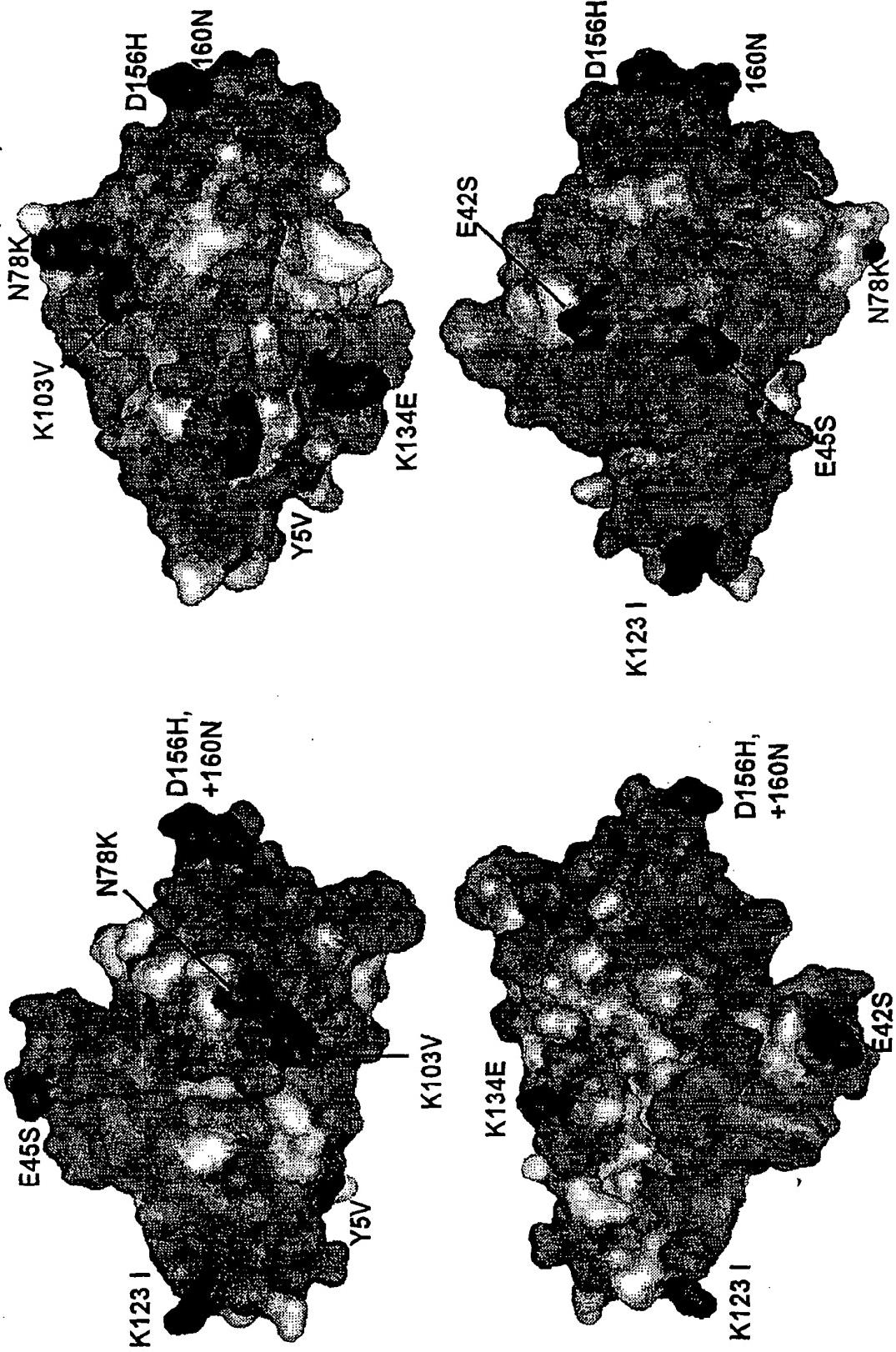


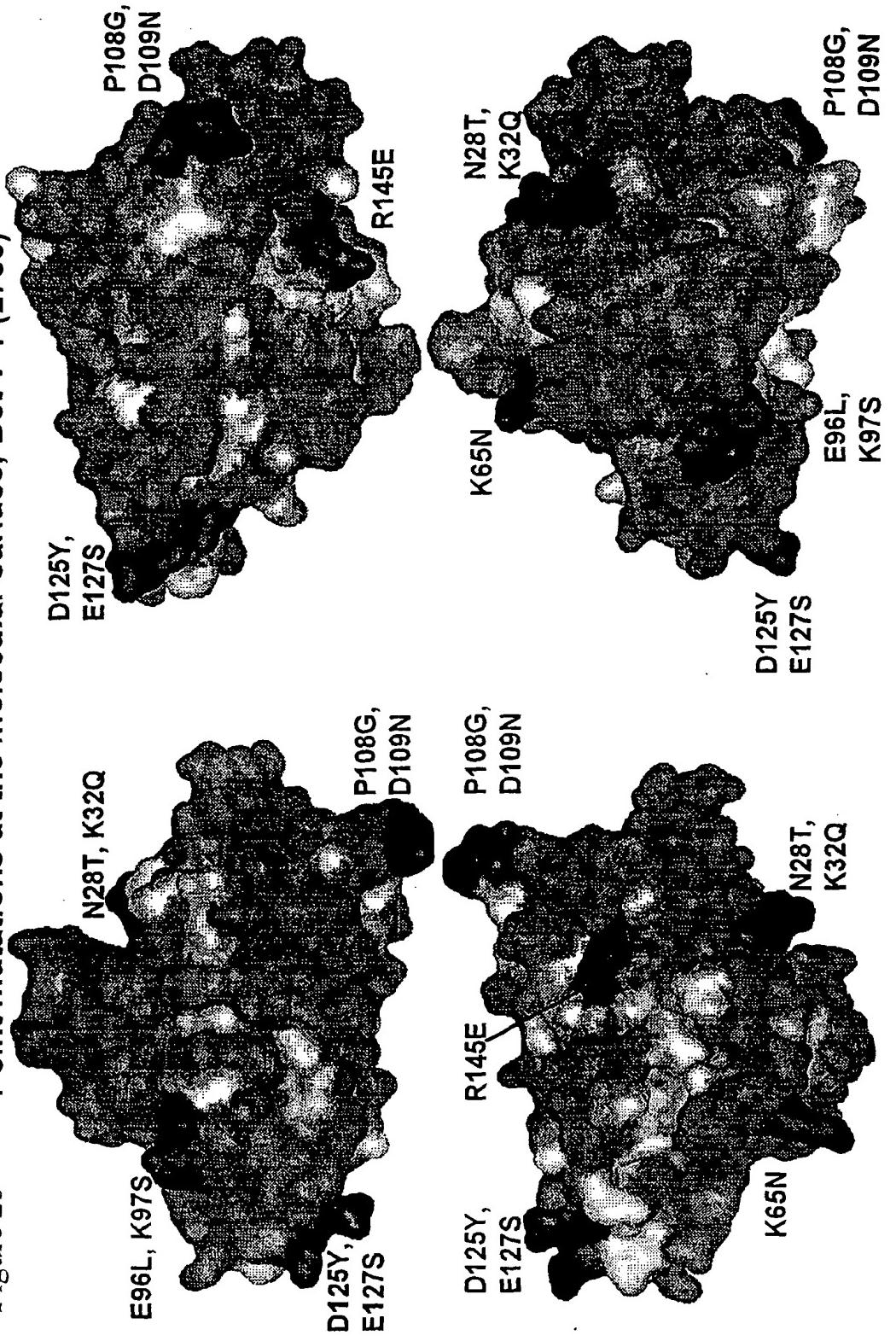
Figure 24

Point mutations at the molecular surface, Bet v 1 (2744)



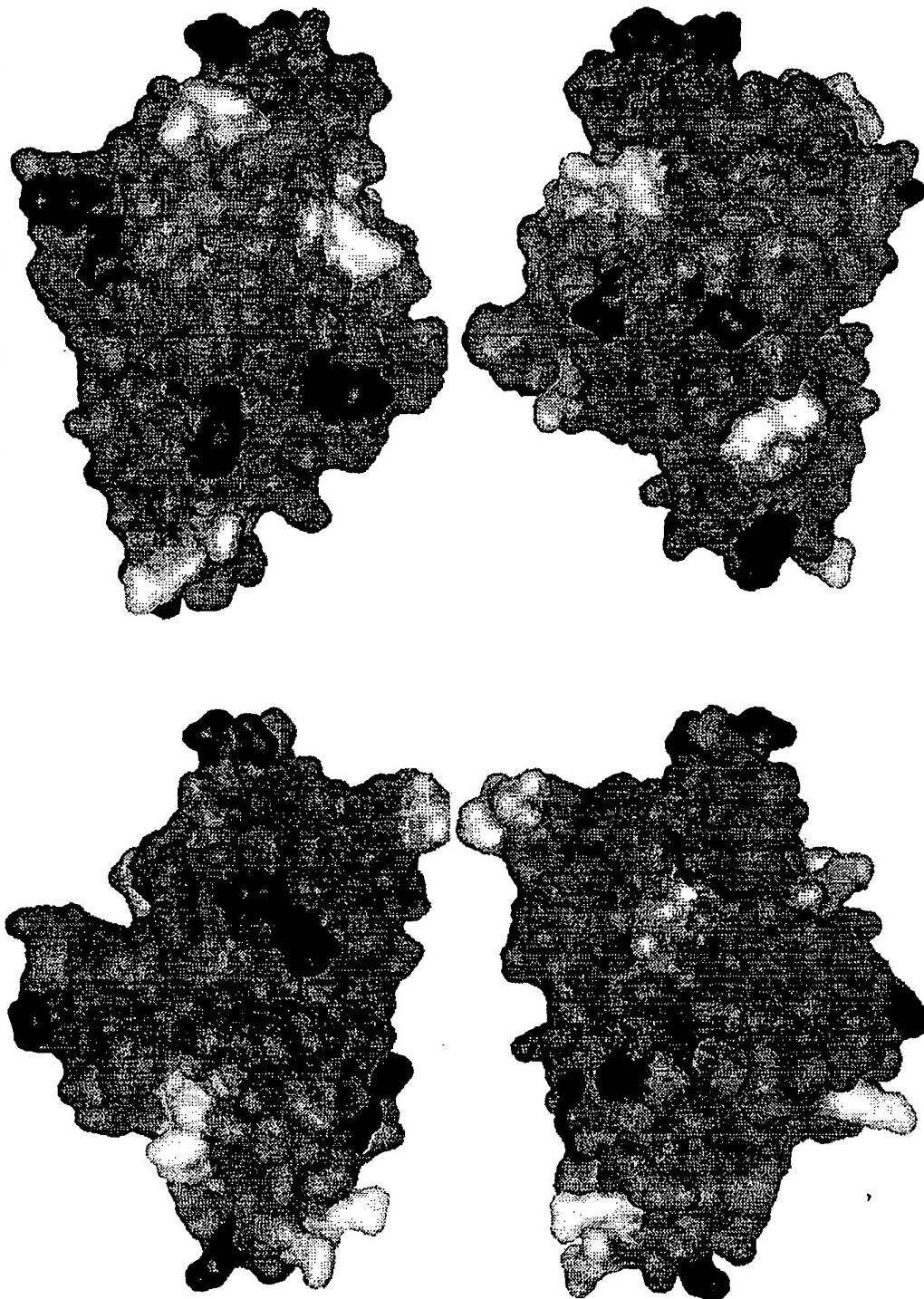
Grey: Back bone + Amino acid residues 95-100% conserved among *Fagales*, Black: Point mutations

Figure 25 Point mutations at the molecular surface, Bet v 1 (2753)



"Y" "F" "G" "P" "T" "W" "C" "H" "R" "Q" "S" "D" "E" "K" "N" "M" "L" "V" "I" "A" "H" "C" "D" "G" "P" "T" "W" "C" "H" "R" "Q" "S" "D" "E" "K" "N" "M" "L" "V" "I" "A"

Distribution of point mutations at the molecular surface of, Bet v-4 (2744) [white], and Bet v 1 (2753) [Black]



Grey: Molecular surface; amino acid residues 95-100% conserved among *Fagales*
Black: Mutations (Y5V, K134E), (E42S, E45S), (N78K, K103V), K123 I, (D156H, +160N)
White: Mutations (N28T, K32Q), K65N, (E96L, K97S), (P108G, D109N), (D125Y, E127S), R145E

Figure 26

Figure 27 Circular dichroism spectra of Bet v 1.2801 and mutant Bet v 1(2744), pH 7.13, T 20C.

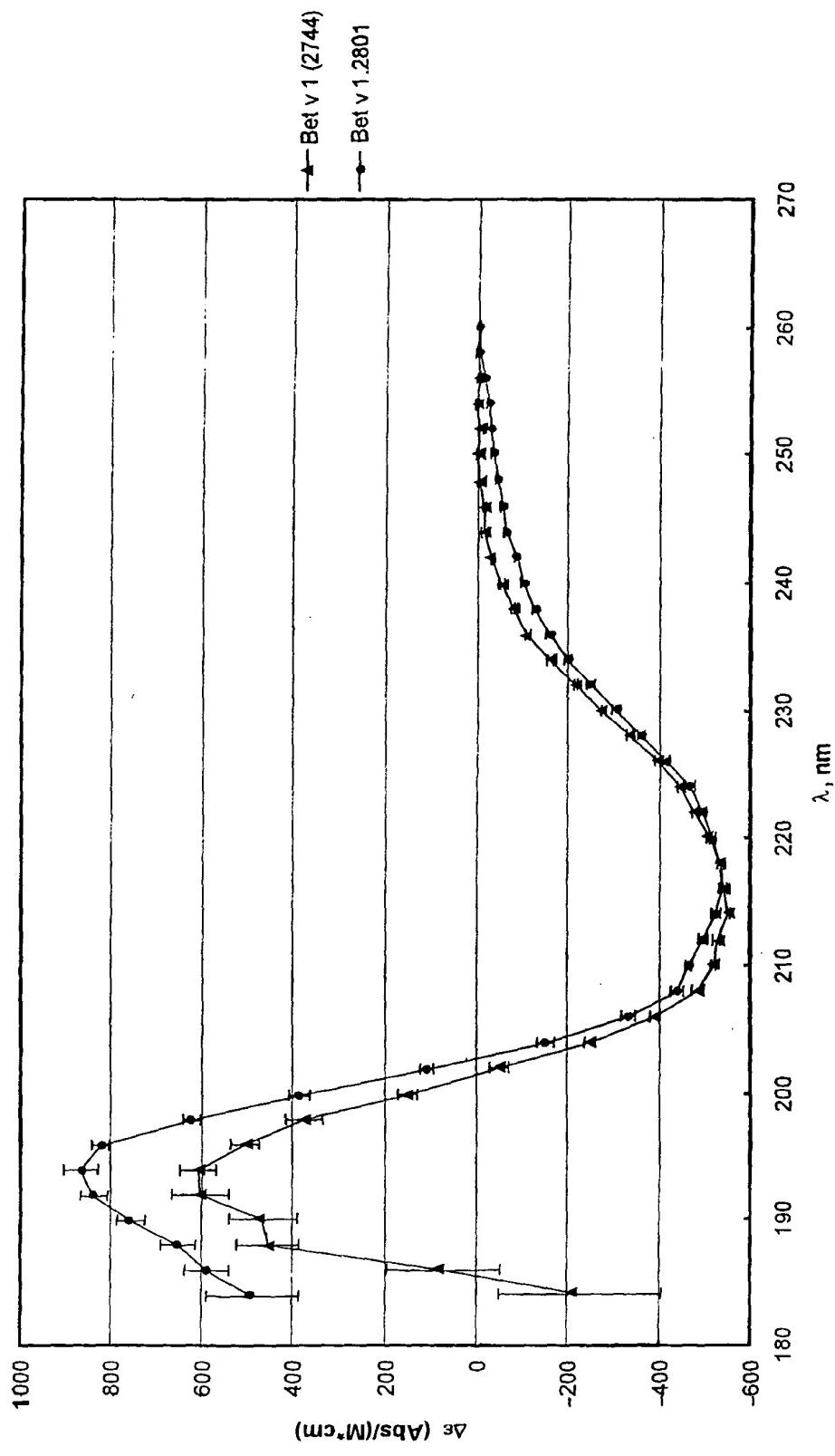
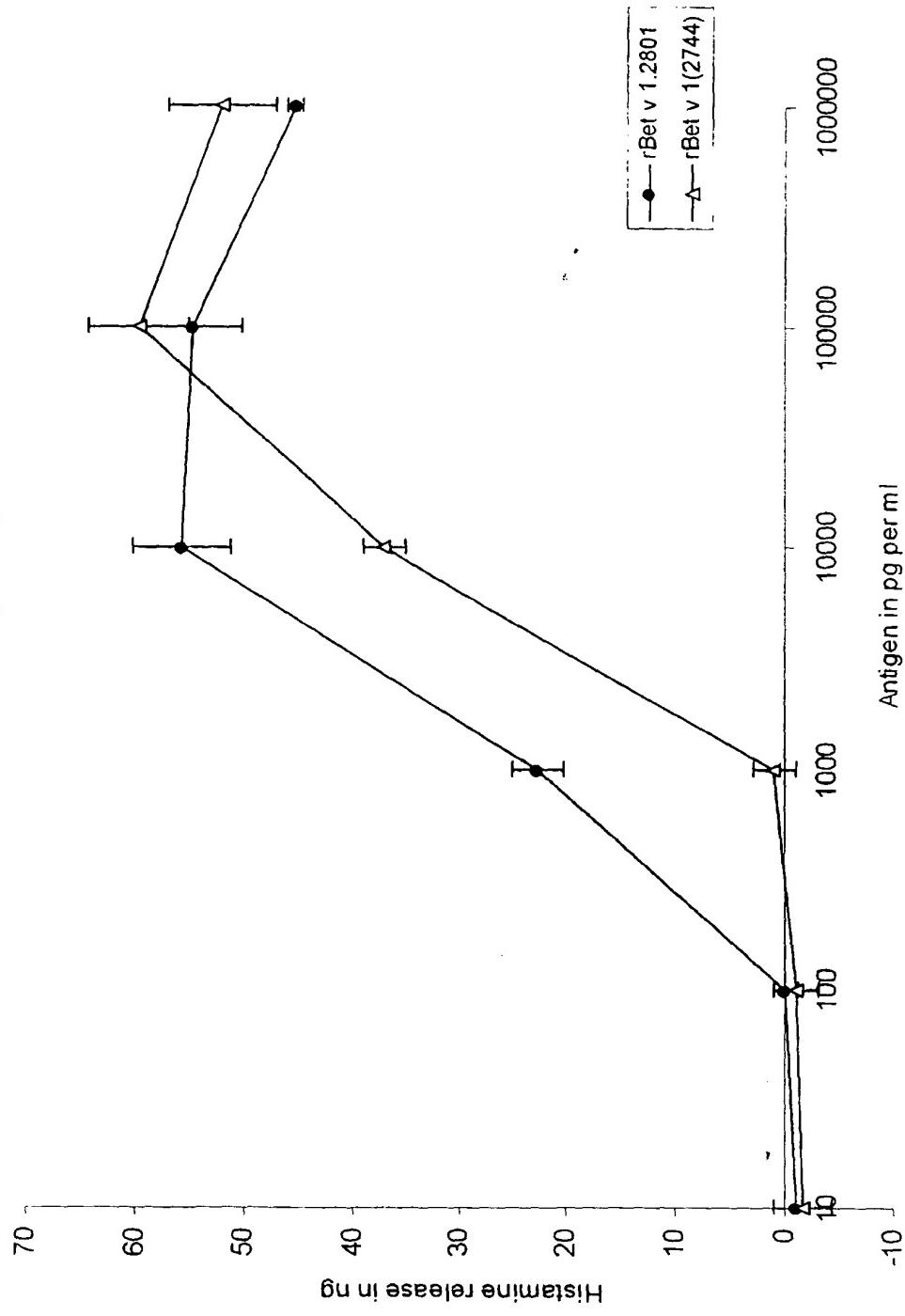


Fig. 28: Histamine release, donor MK, Bet v 1.2801 and Bet v 1(2744)



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Fig. 29A: Histamine release, donor MJ, Bet v 1.2801 and Bet v 1 (2744)

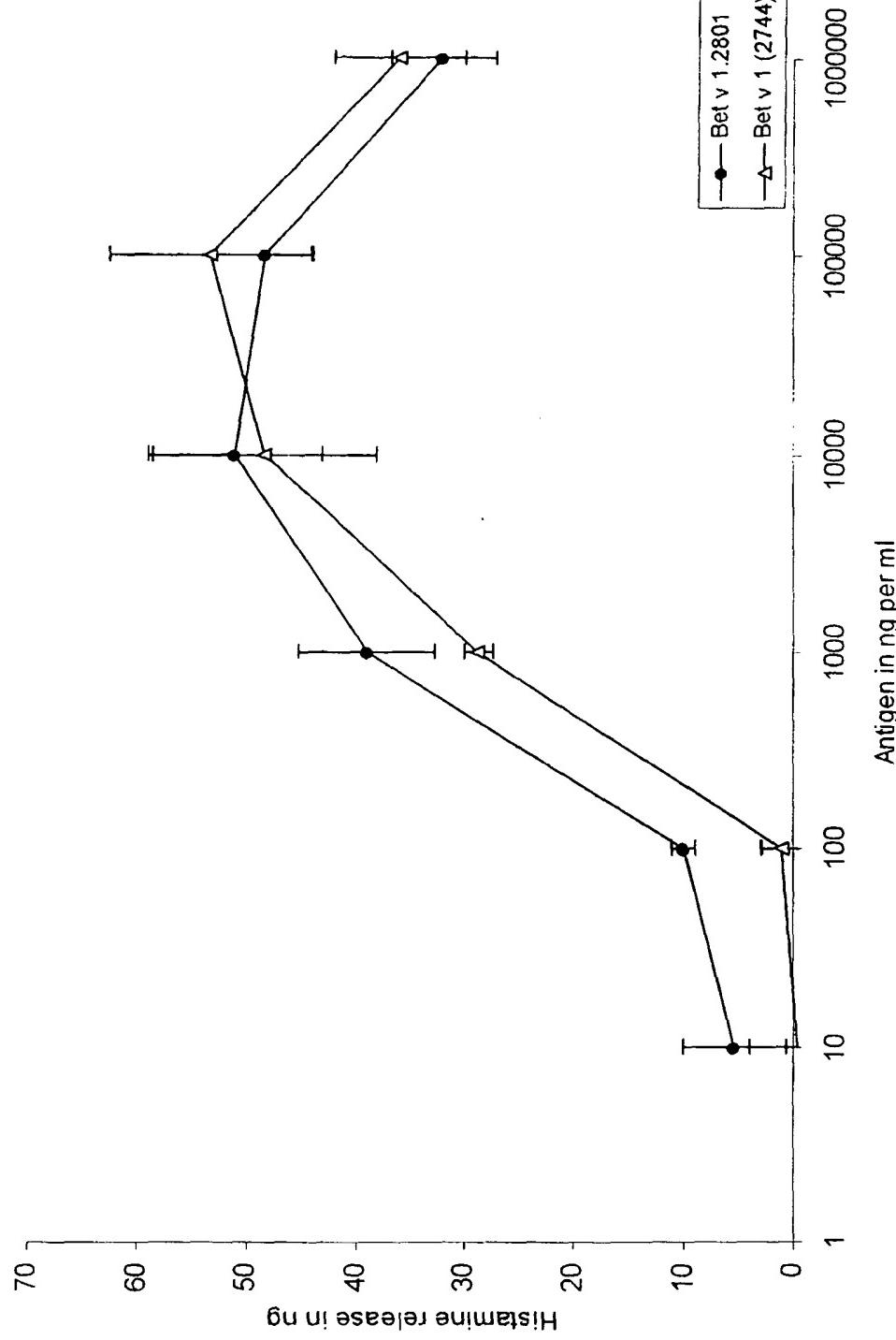
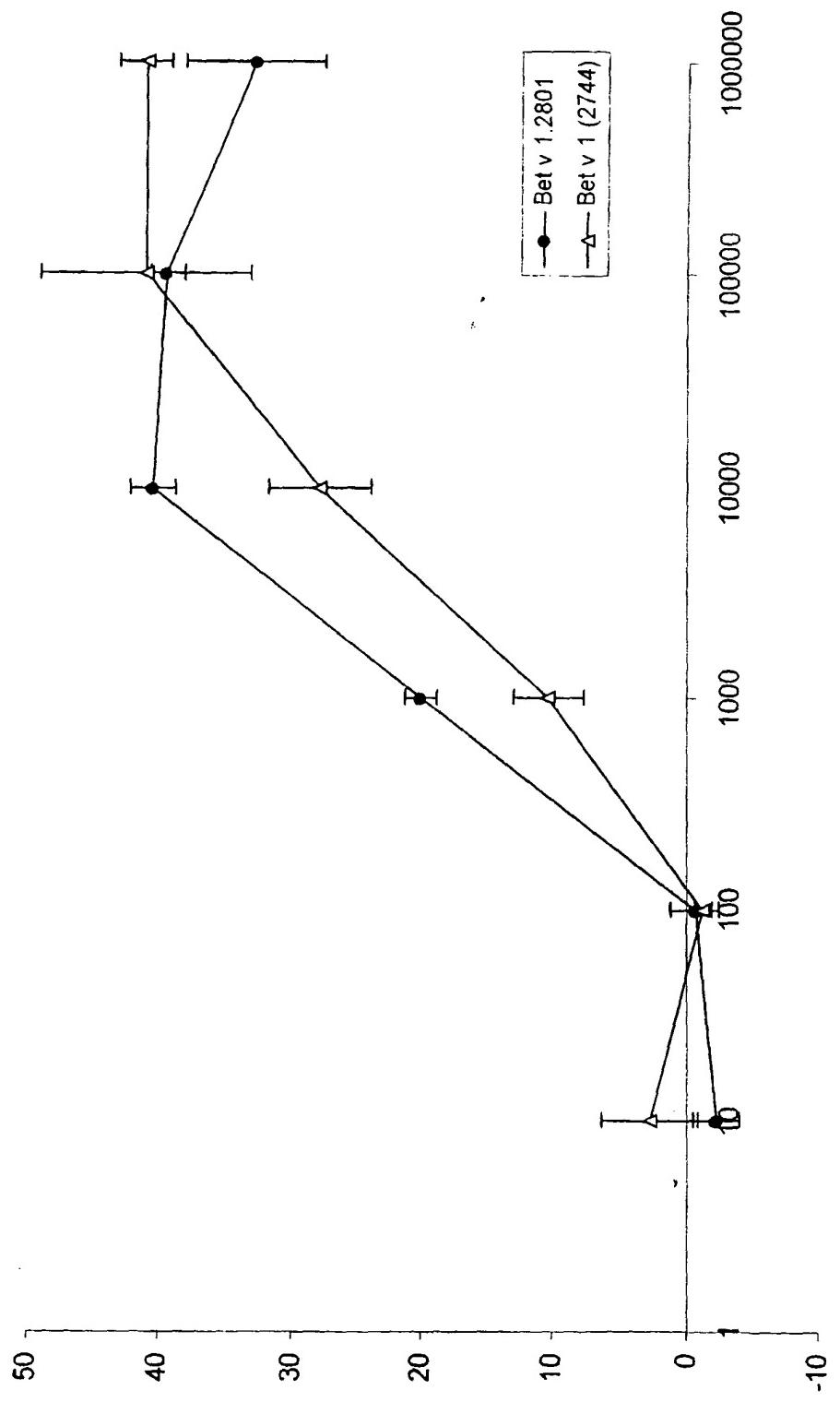


Fig.29B: Histamine release, donor MH, Bet v 1.2801 and Bet v 1 (2744)



• 3 2 1 0 -1 2 3 4 5 6

Fig. 29C: Histamine release, donor CJB, Bet v 1.2801 and Bet v 1 (2744)

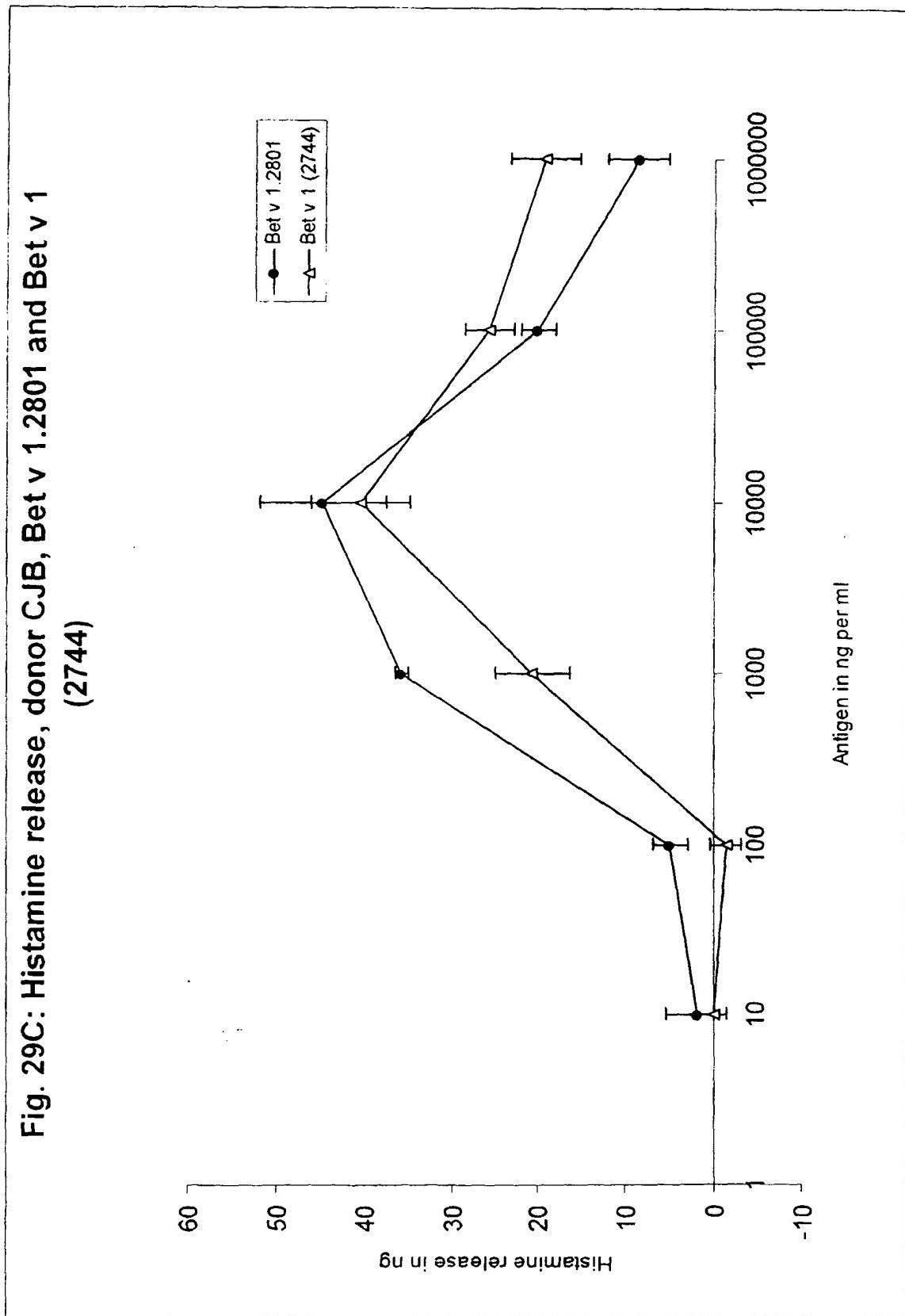
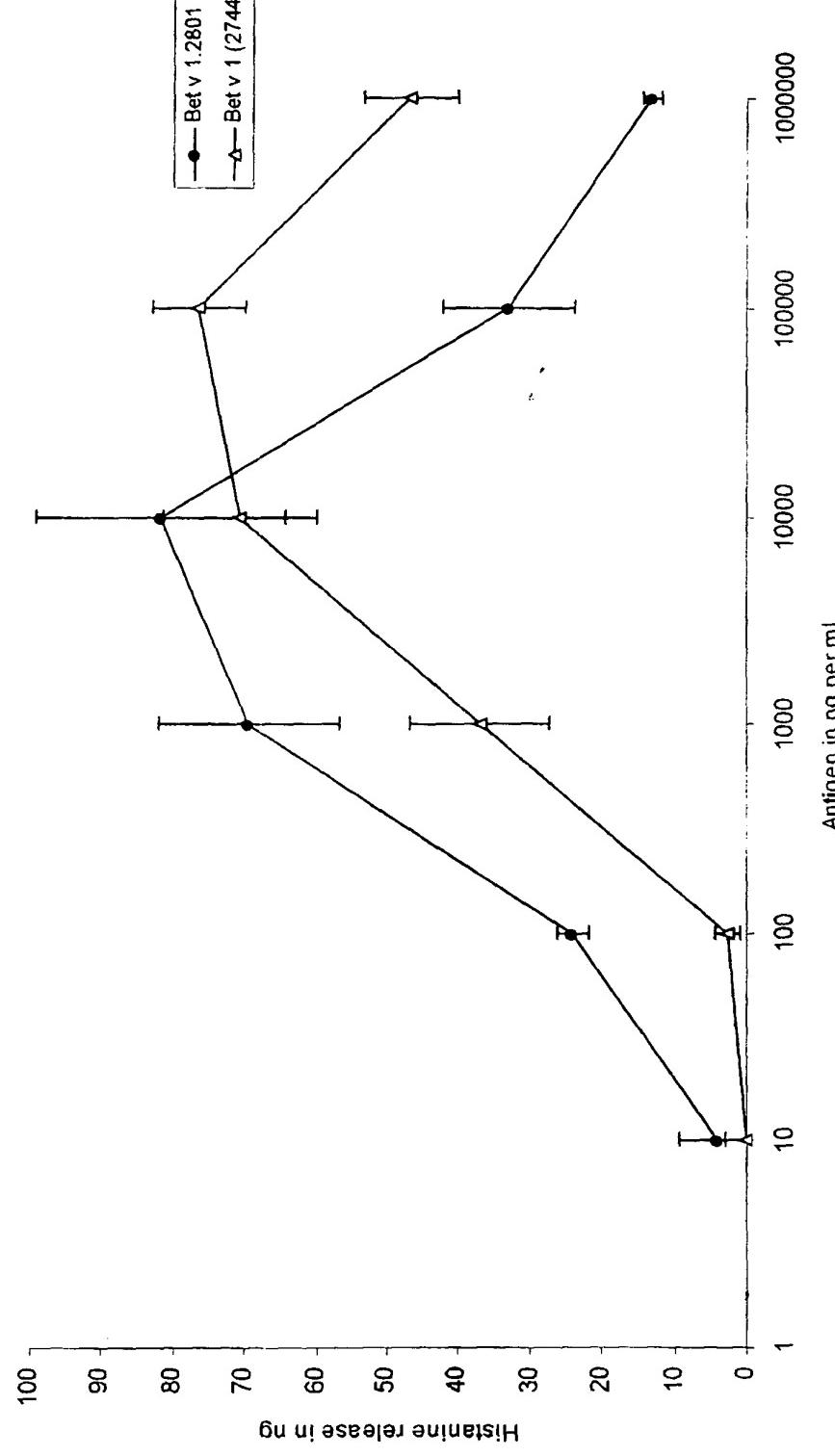
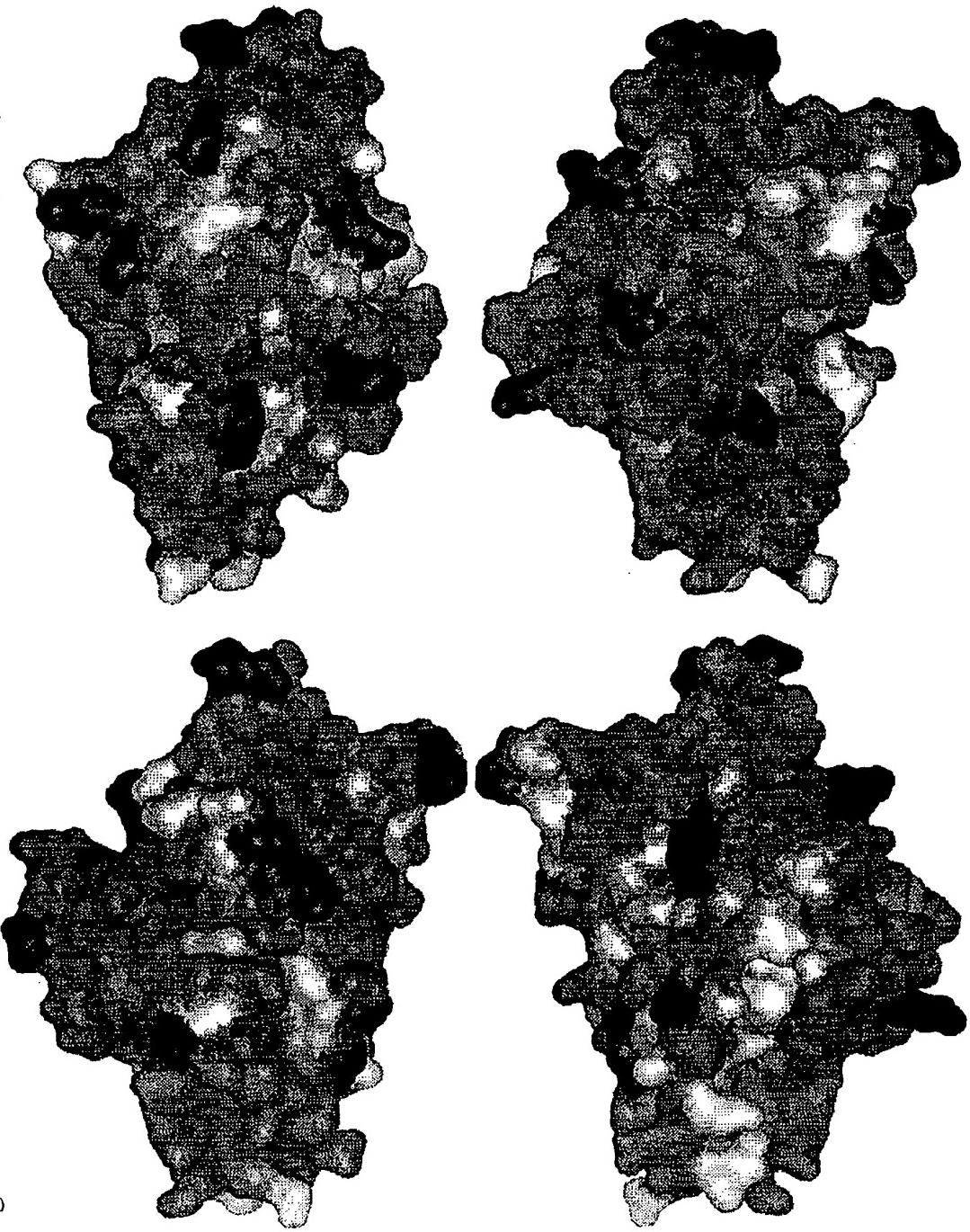


Fig. 29D: Histamine release, donor MCDS, Bet v 1.2801 and Bet v 1 (2744)



ZACCO
HOFMAN-BANG ZACCO

Figure 30 Point mutations at the Molecular surface, Bet v 1 (2733)

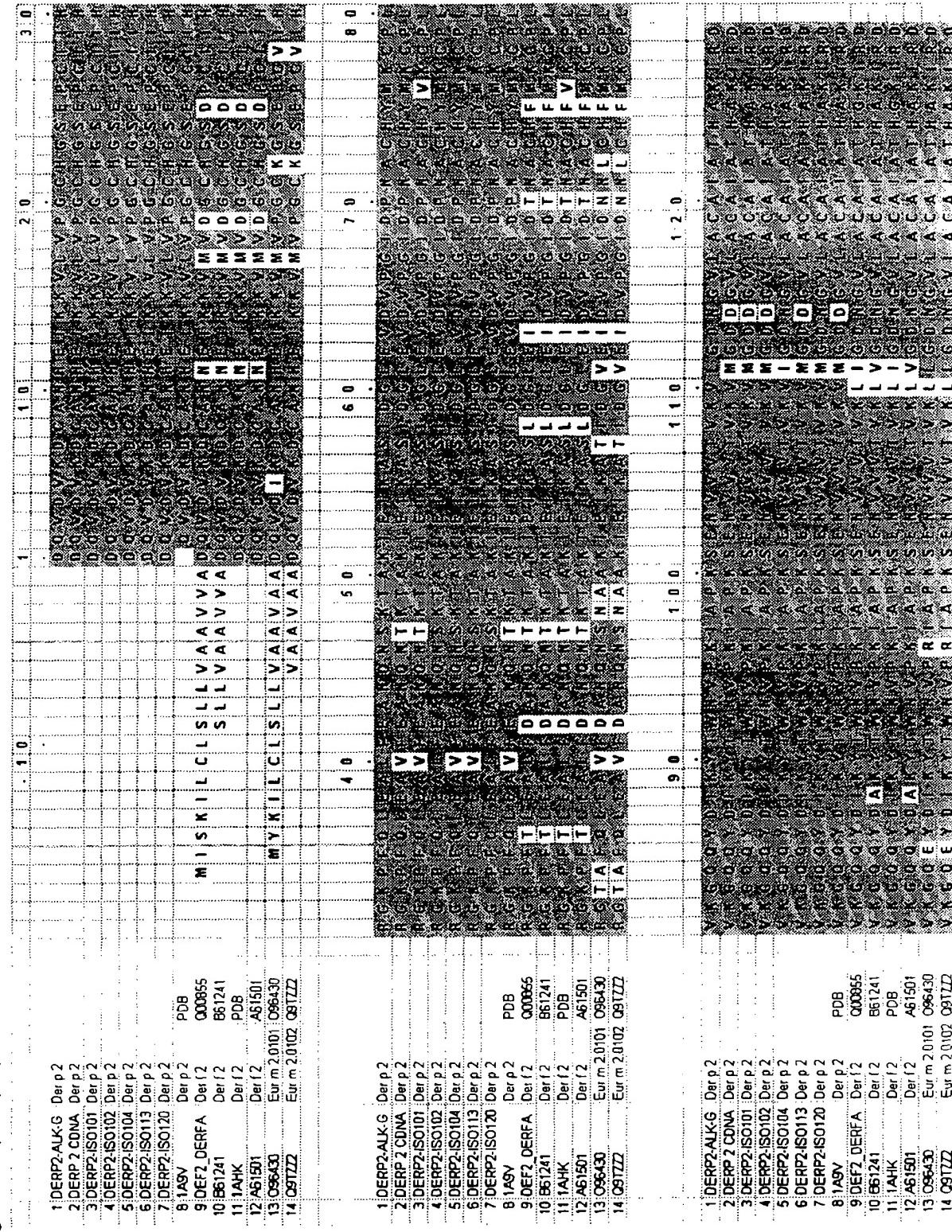


Grey: Backbone + Amino acid residues 95-100% conserved among Fagales,
Black: Point mutations: Y5V, N28T, K32Q, E45S, K65N, N78K, K97S, K103V, P108G, K134E, R145E, D156H, +160N

Figure 31

Oligonucleotide primers for site-directed mutagenesis of Der p 2

K6A	sense	OB43	42-mer	5' -CCG <u>CTCGAG</u> AAAAGAGAGATCAAGTCGATGTCGCCGATTGTGCC- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'
K15E	sense	OB44	67-mer	5' -CCG <u>CTCGAG</u> AAAAGAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTCG- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'
H30N	sense	OB46	54-mer	5' -CGGGGTAC <u>CCAGGAT</u> GTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTAT <u>CAGTTGATGTTCCC</u> - 3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC- 3'
H74N	sense	OB49	32-mer	5' -CAT <u>GGCATGCAATTACATGAAATGCCATTGG</u> - 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'
K82N	sense	OB50	50-mer	5' -CTAC <u>GCATGCCATTACATGAAATGCCATTGGTTAATGGACAA</u> CAATATG- 3'
	anti-sense	OB28	39-mer	5' -CGT <u>CTAGACT</u> ATTAATCGCGGATTTAGCATGAGTTGC- 3'



4 0 0 1 2 4 E - 4 0 0 1 2 4

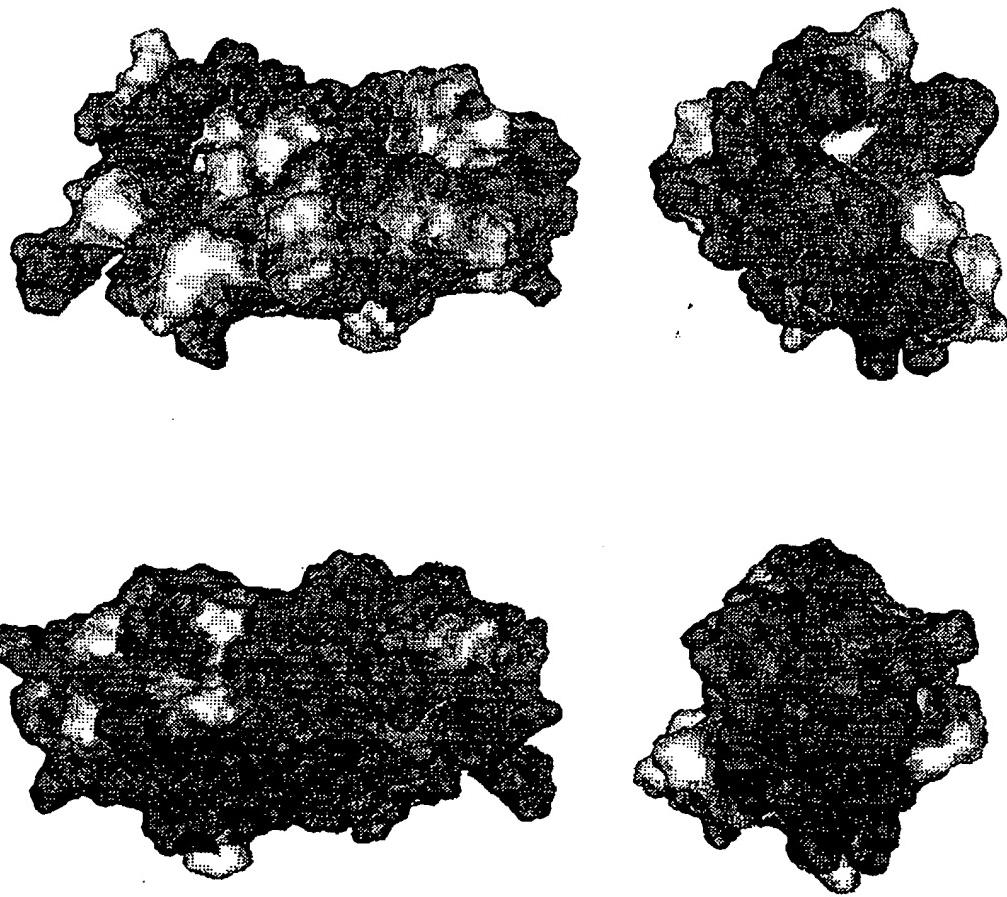


FIG. 33: Der p 2

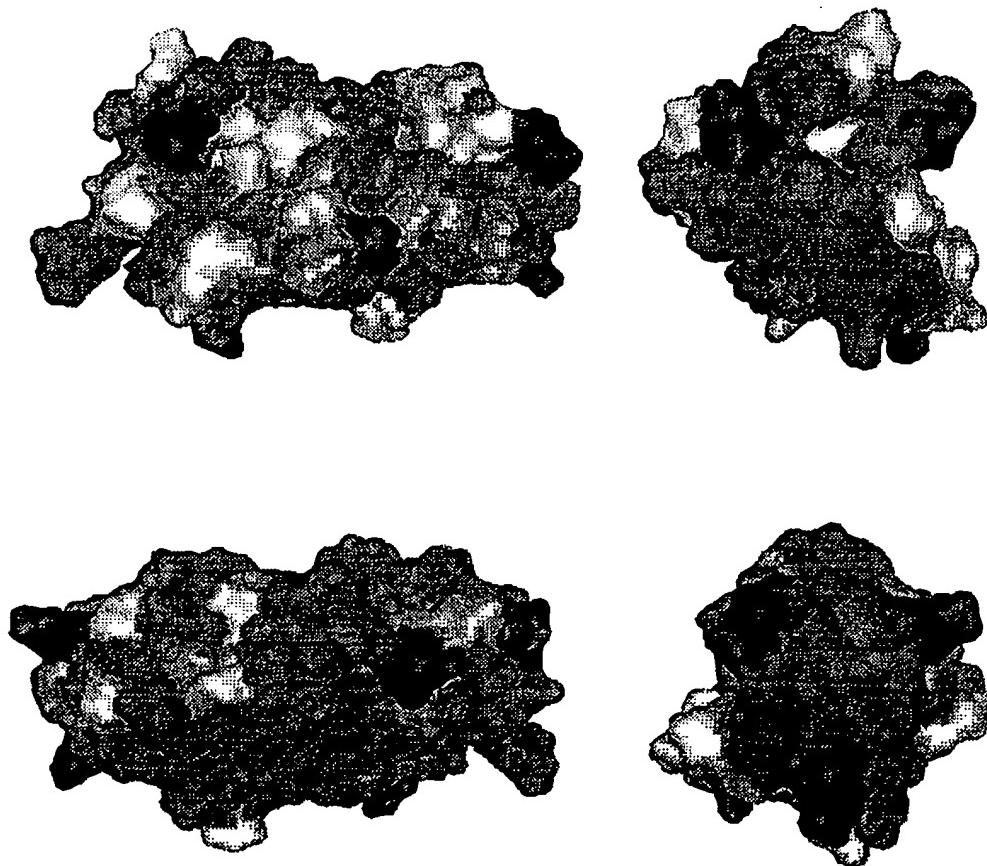


FIG. 34: Der p 2 mutant

Figure 35A (Der p 1)

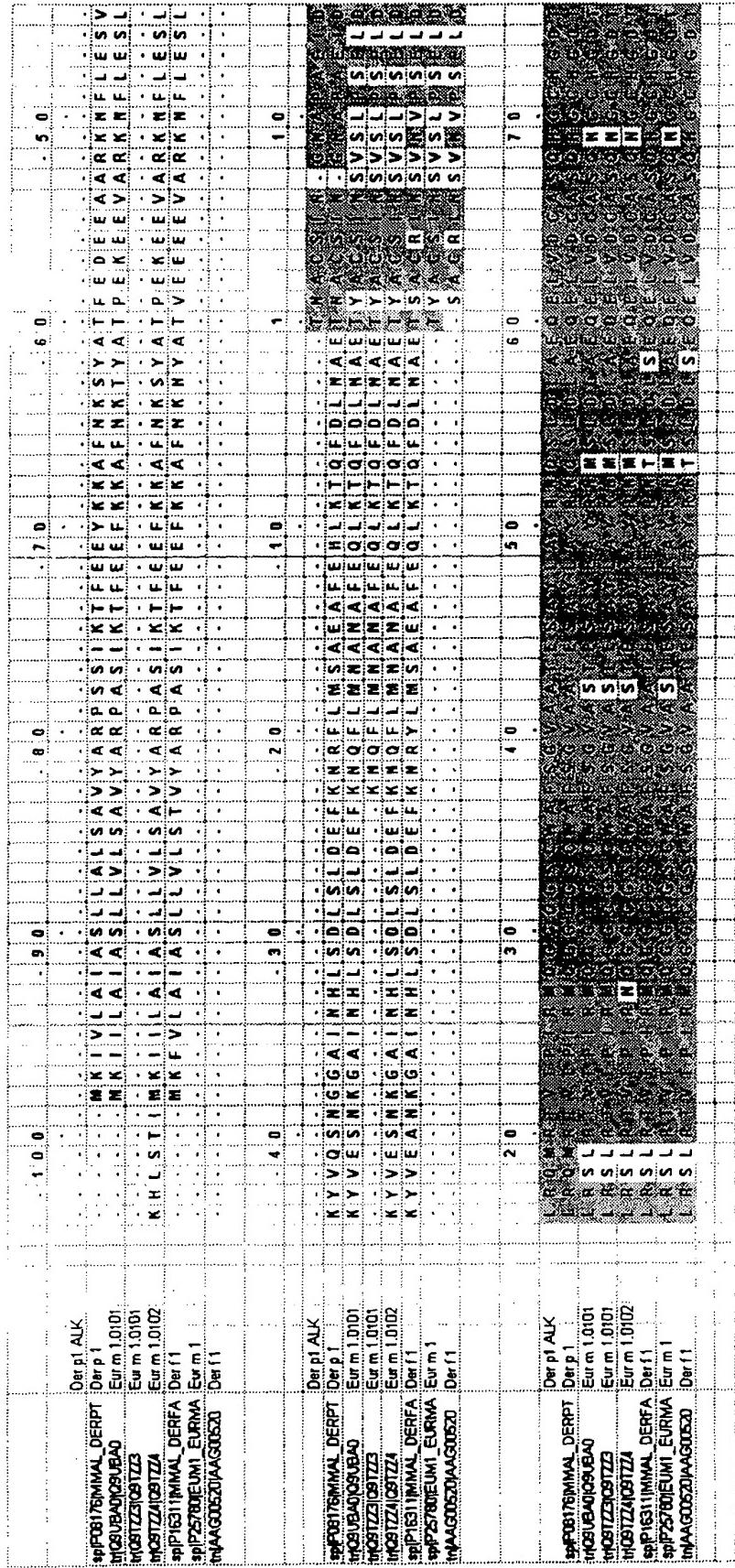
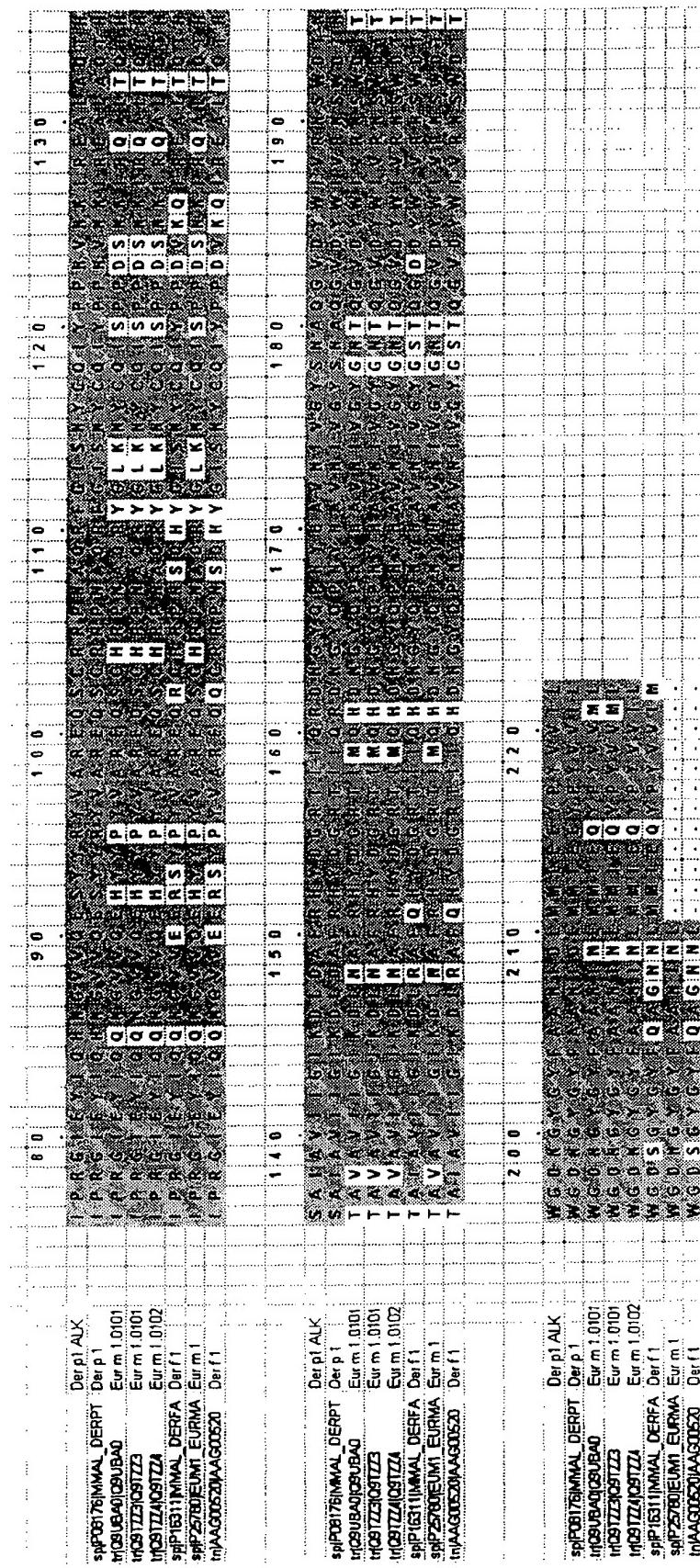


Figure 35B (Der p 1)



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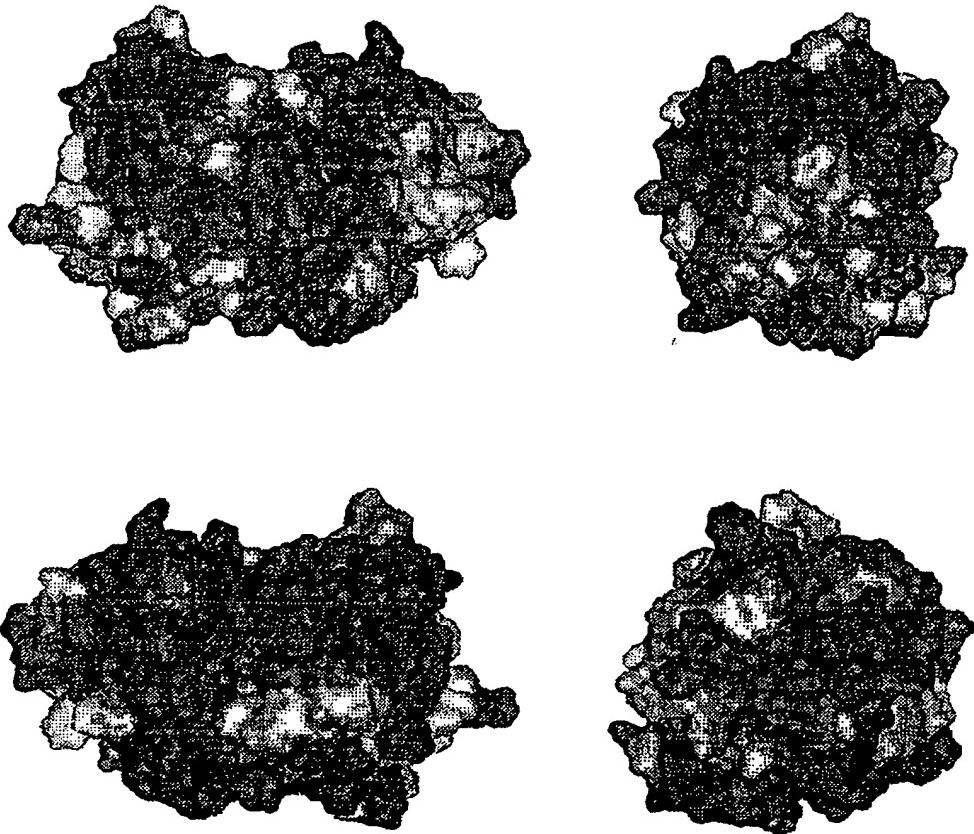


FIG. 36: Der p 1

363245 a 3534

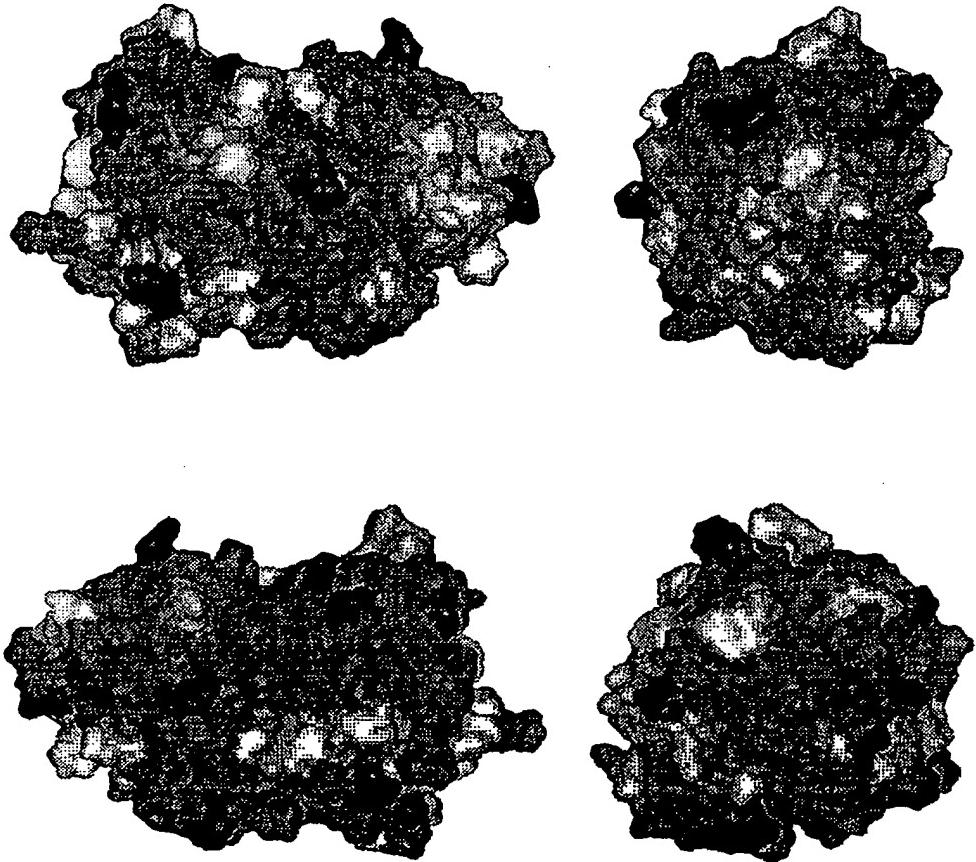


FIG. 37: Der p 1 mutant

FIG. 38A (Ph1 p 5)

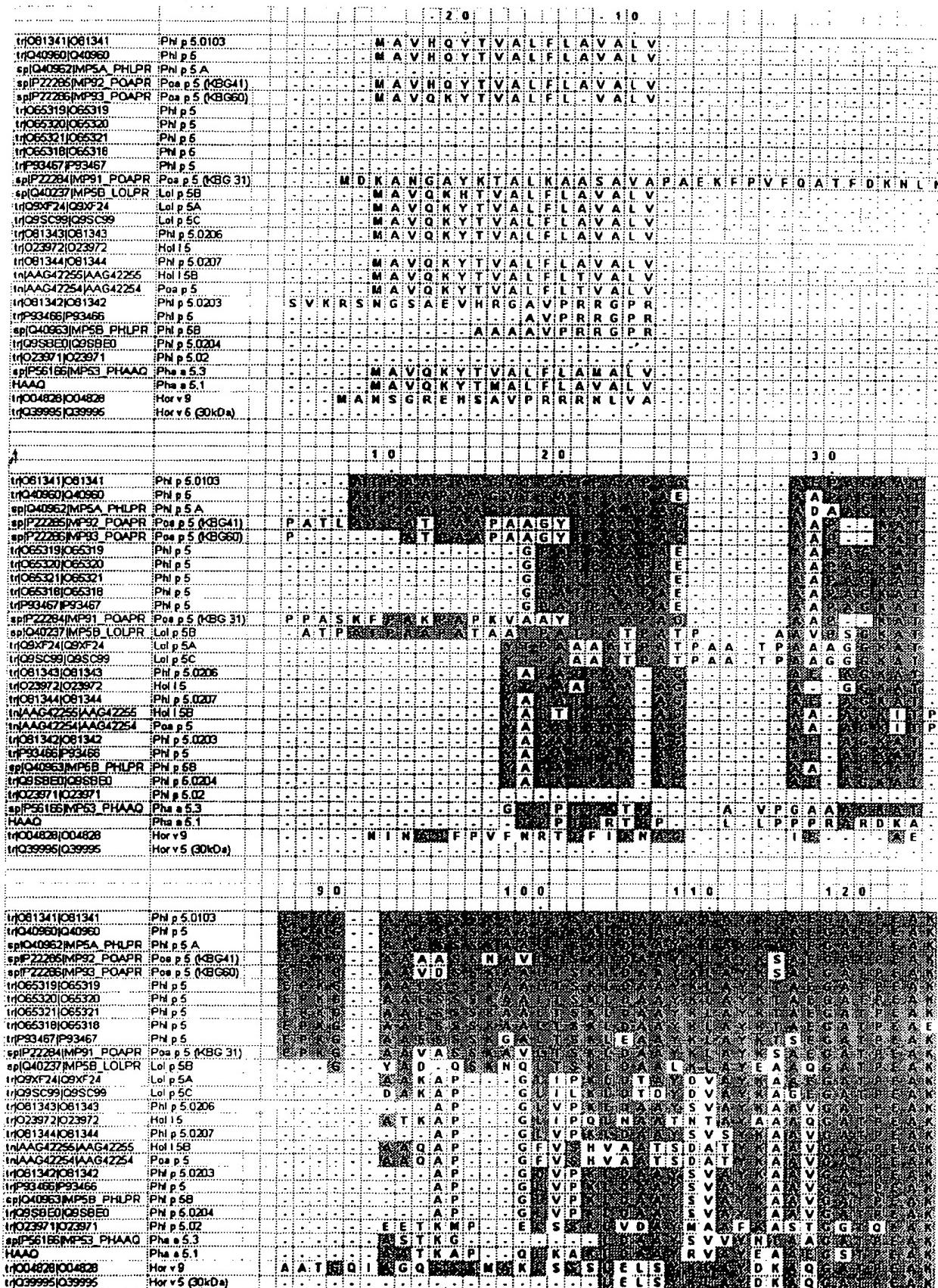


FIG. 38B (PhI p 5)

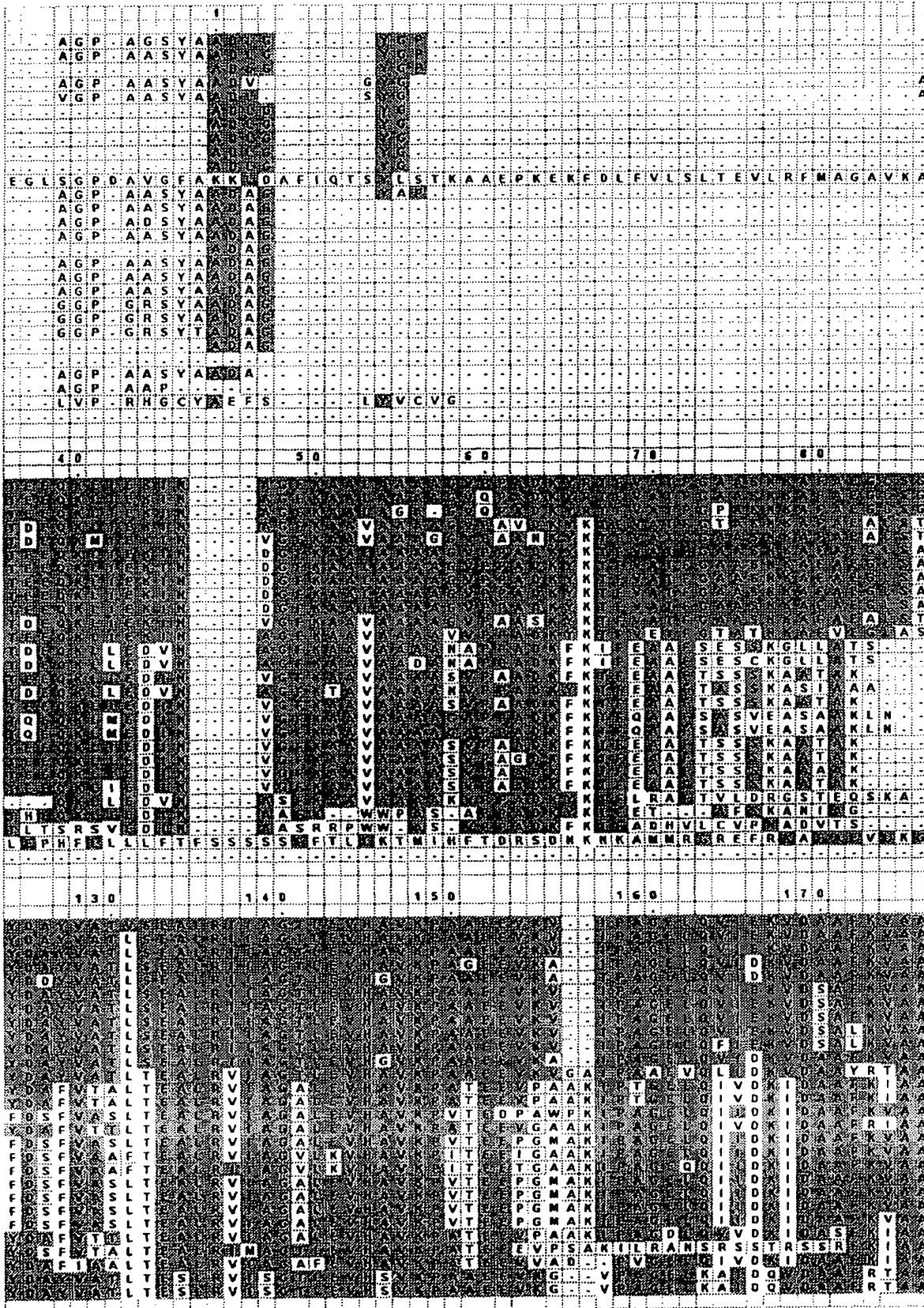
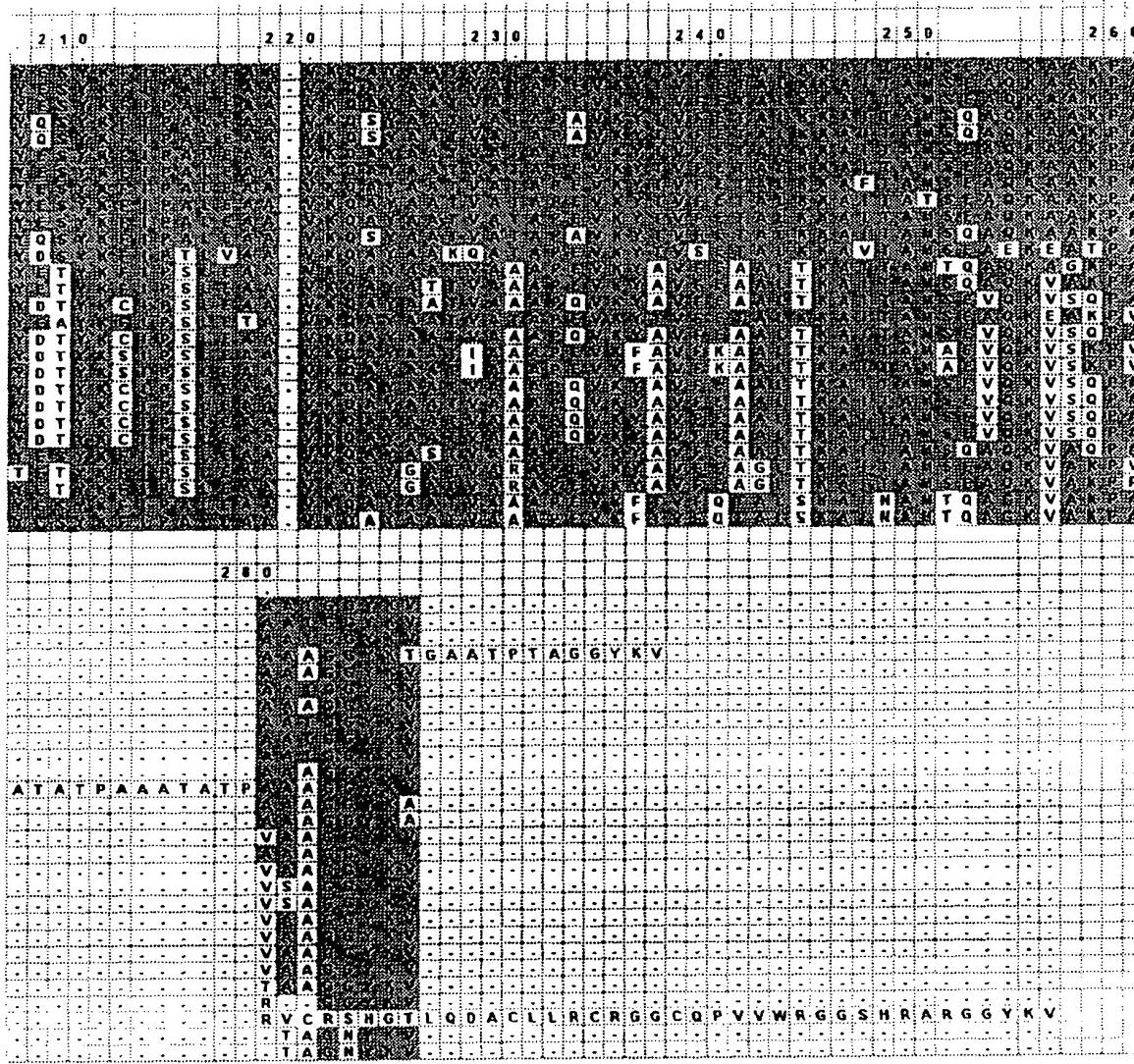


FIG. 38C (Phl p 5)

			1 0 0		1 0 0		2 0 0
tr O81341 O81341	Pho p 5.0103	- - - - -					
tr O40960 O40960	Pho p 5	- - - - -					
sp Q40562 MP56_PHLPR	Pho p 5 A	- - - - -					
sp P22226 MP52_POAPR	Poa p 5 (KBG41)	- - - - -					
sp P22226 MP53_POAPR	Poa p 5 (KBG50)	- - - - -					
tr O65319 O65319	Pho p 5	- - - - -					
tr O65321 O65321	Pho p 5	- - - - -					
tr O65318 O65318	Pho p 5	- - - - -					
tr P93467 P93467	Pho p 5	- - - - -					
sp P22224 MP31_POAPR	Poa p 5 (KBG 31)	- - - - -					
sp P40023 MP56_LOUPR	Lol p 5B	- - - - -					
tr O9xF24 O9xF24	Lol p 5A	- - - - -					
tr O9xC99 O9xC99	Lol p 5C	- - - - -					
tr O81343 O81343	Pho p 5.0206	- - - - -					
tr O23972 O23972	Hol 15	- - - - -					
tr O81344 O81344	Pho p 5.0207	- - - - -					
tr IAAG4225 IAAG4225	Hol 15B	- - - - -					
tr IAAG4225 IAAG4225	Pho p 5	- - - - -					
tr O61342 O61342	Pho p 5.0203	- - - - -					
tr P93465 P93465	Pho p 5B	- - - - -					
tr O9xB60 O9xB60	Pho p 5.0004	- - - - -					
tr O23971 O23971	Pho p 5.02	- - - - -					
sp P95165 MP53_PHAAQ	Pho p 5.3	T I V A I T P L S H S	S	S	T	R	L
HAAG	Pho p 5.1	- - - - -	D	D	G	K	E R H A
tr O046528 O046528	Hor v 8	- - - - -	D	D	G	O G P S	R K P R G
tr Q39995 Q39995	Hor v 5 (OKOa)	- - - - -	D	D	G	O G P S	R K P R G
tr O81341 O81341	Pho p 5.0103	- - - - -					
tr O40960 O40960	Pho p 5	- - - - -					
sp Q40562 MP56_PHLPR	Pho p 5 A	- - - - -					
sp P22226 MP52_POAPR	Poa p 5 (KBG41)	- - - - -					
sp P22226 MP53_POAPR	Poa p 5 (KBG50)	- - - - -					
tr O65319 O65319	Pho p 5	T E - - -	G	G A V G A A T			
tr O65320 O65320	Pho p 5	T E - - -	S				
tr O23972 O23972	Pho p 5	T E - - -					
tr O65318 O65318	Pho p 5	T E - - -					
tr P93467 P93467	Pho p 5	T E - - -					
sp P22224 MP31_POAPR	Poa p 5 (KBG 31)	- - - - -	V G P S P A A T	A T F A A A Y A T	P A A A T		
sp P40023 MP56_LOUPR	Lol p 5B	- - - - -	A A G A V T	A T G - - -	A A A A G		
tr O9xF24 O9xF24	Lol p 5A	- - - - -	A A G A V T	A T G - - -	A A A A G		
tr O9xC99 O9xC99	Lol p 5C	- - - - -	A A G A V T	A T G - - -	A A A A G		
tr O81343 O81343	Pho p 5.0206	T G - - -	A A V A A G	T T T G	A A A A G		
tr O23972 O23972	Hol 15	- - - - -	A A V A A G	T T T G	A A A A G		
tr O81344 O81344	Pho p 5.0207	T G - - -	A A V A A G	T T T G	A A A A G		
tr IAAG4225 IAAG4225	Hol 15B	- - - - -	A A V A A G	T T T G	A A A A G		
tr IAAG4225 IAAG4225	Pho p 5	- - - - -	A A V A A G	T T T G	A A A A G		
tr O046528 O046528	Pho p 5.0203	T G - - -	A A V A A G	T T T G	A A A A G		
tr P93465 P93465	Pho p 5	- - - - -	A A V A A G	T T T G	A A A A G		
tr P40562 MP56_PHLPR	Pho p 5B	- - - - -	A A V A A G	T T T G	A A A A G		
tr O9xB60 O9xB60	Pho p 5.0204	T G - - -	A A V A A G	T T T G	A A A A G		
tr O23971 O23971	Pho p 5.02	- - - - -	A A V A A G	T T T G	A A A A G		
sp P95165 MP53_PHAAQ	Pho p 5.3	R L S P Q -	F P O V L P L	I G - - -	V A A A S D S		
HAAG	Pho p 5.1	- - - - -	F P O V L P L	I G - - -	V A A A S D V		
tr O046528 O046528	Hor v 8	- - - - -	V A A A S D S				
tr Q39995 Q39995	Hor v 5 (OKOa)	- - - - -	V A A A S D V				

FIG. 38D (Phl p 5)



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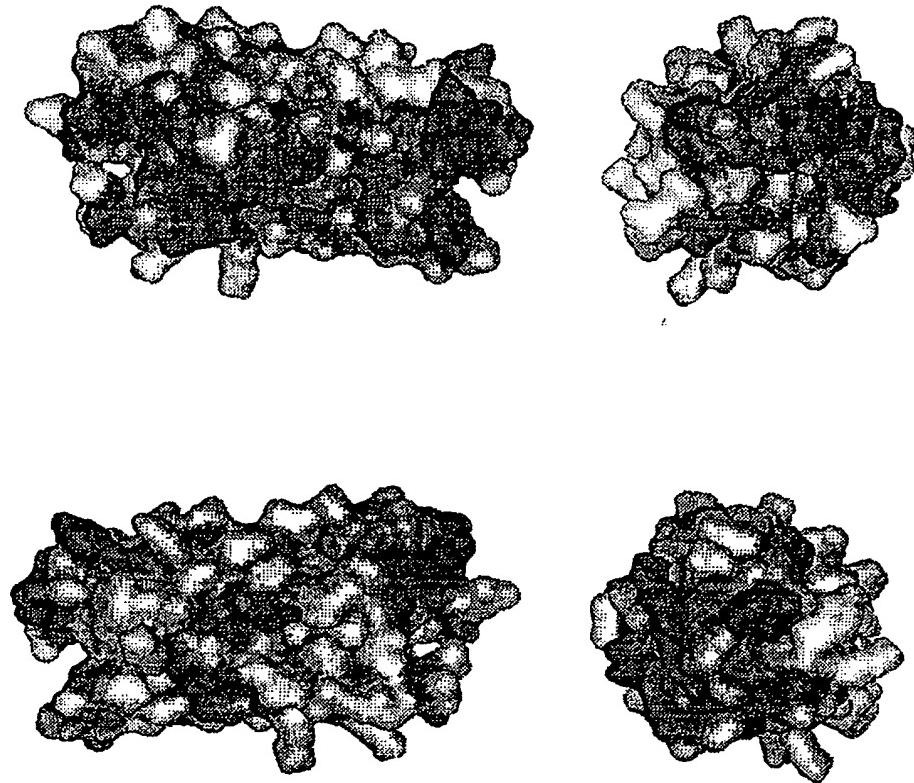


FIG. 39A: Ph1 p 5, Model A

PLATE 39B PHILADELPHIA MUSEUM OF NATURAL HISTORY

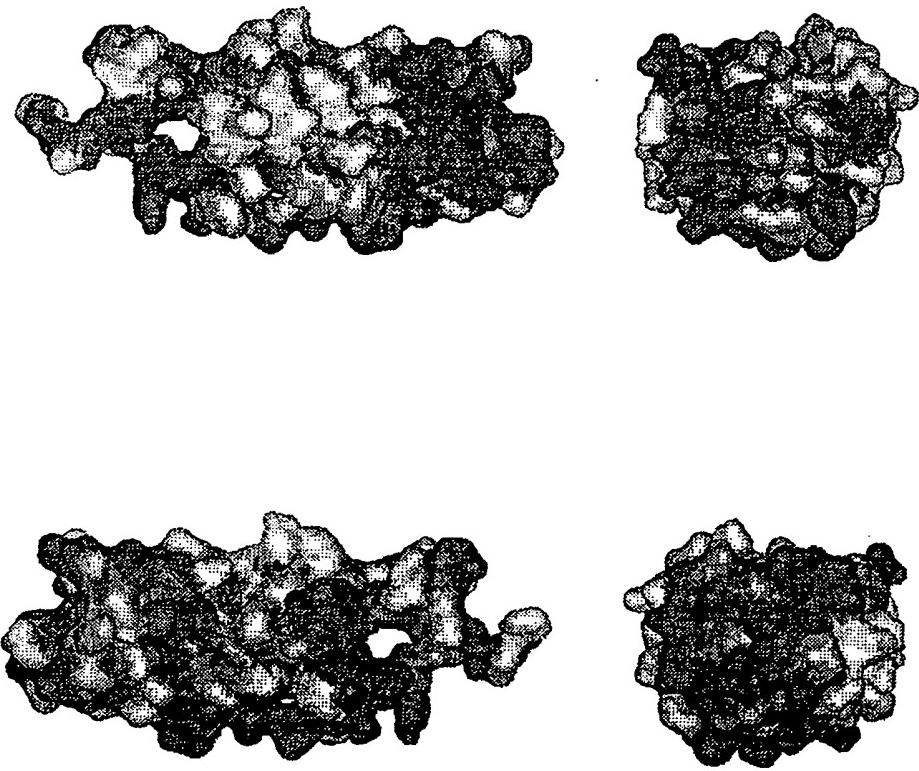


FIG. 39B: Phl p 5, Model B

40A

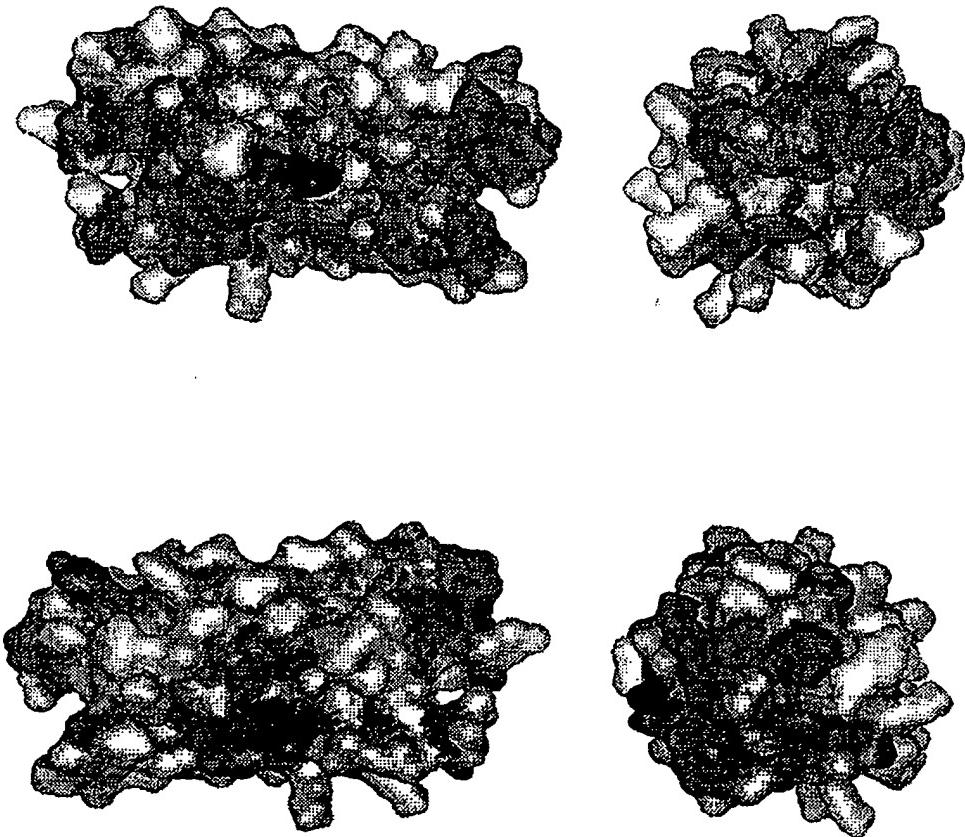


FIG. 40A: Phl p 5 mutant, Model A

40B-1245-A3A583

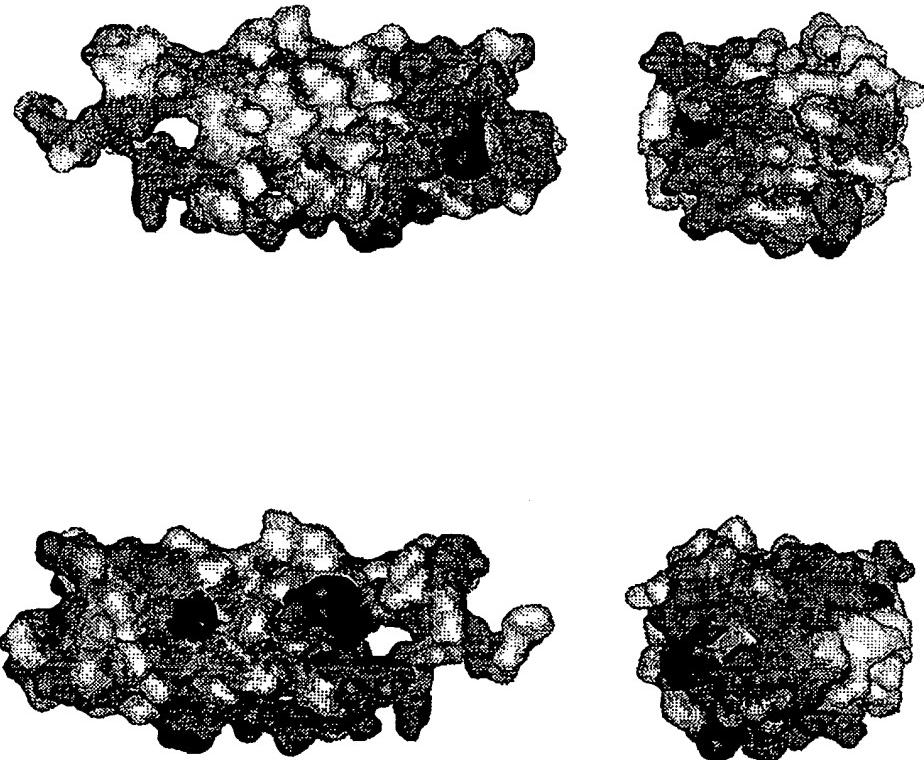


FIG. 40B: Phl p 5 mutant, Model B

2595 2628 2637 2744 2773 PPD

Bet v 1-specific proliferation in patient PBL

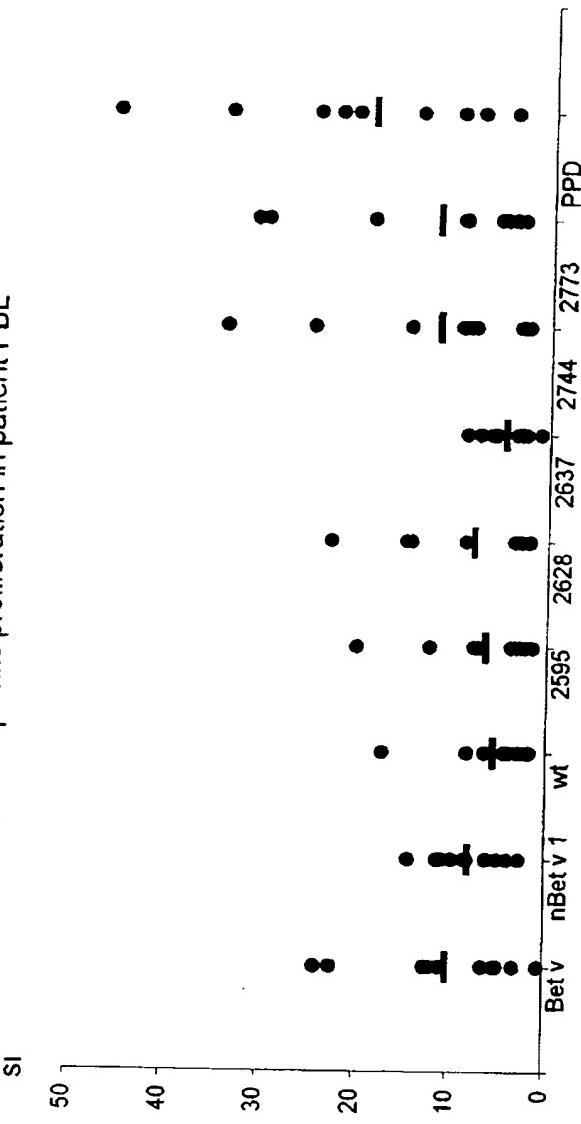


Figure 41: Stimulation of Bet v 1 samples

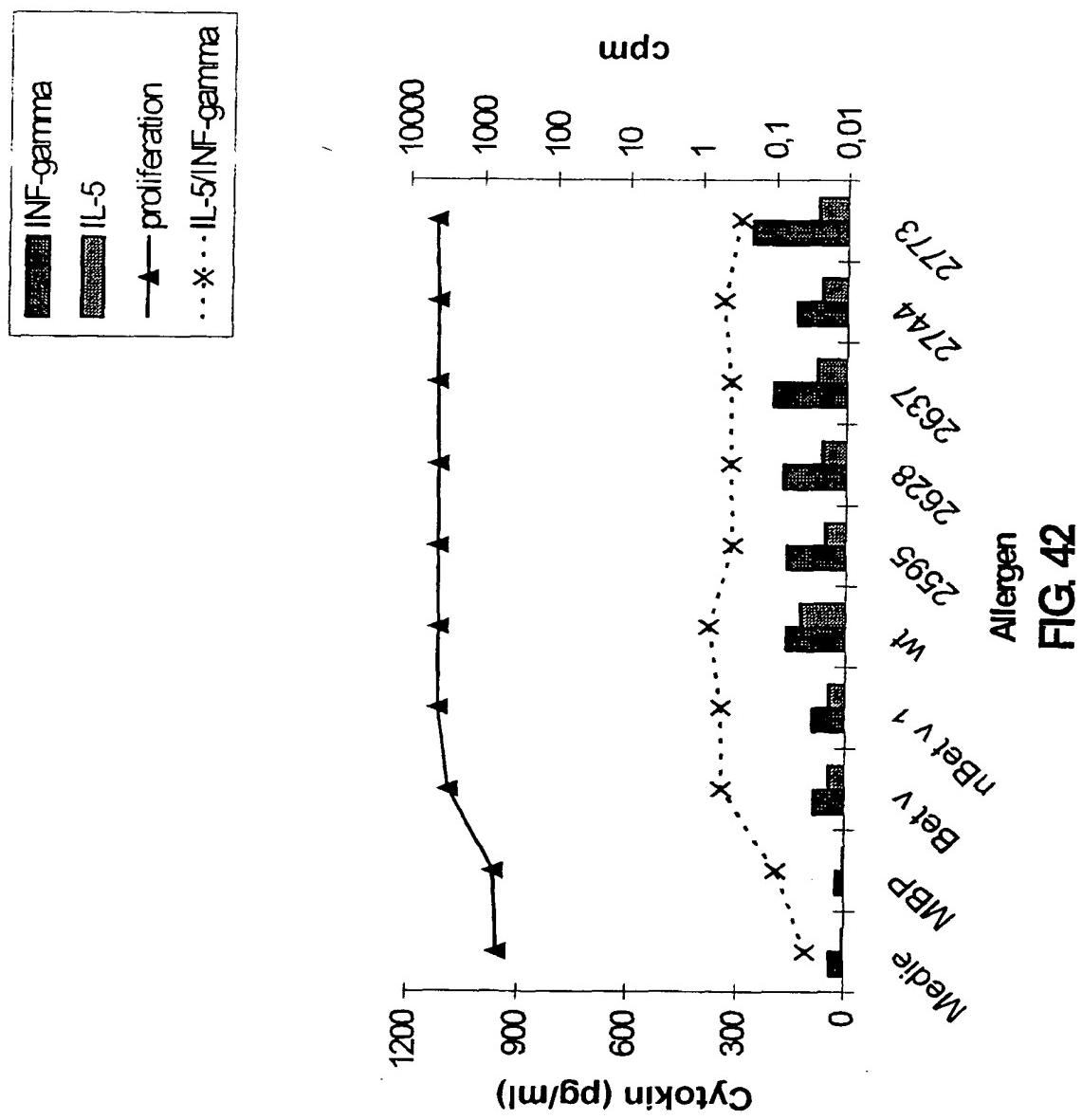
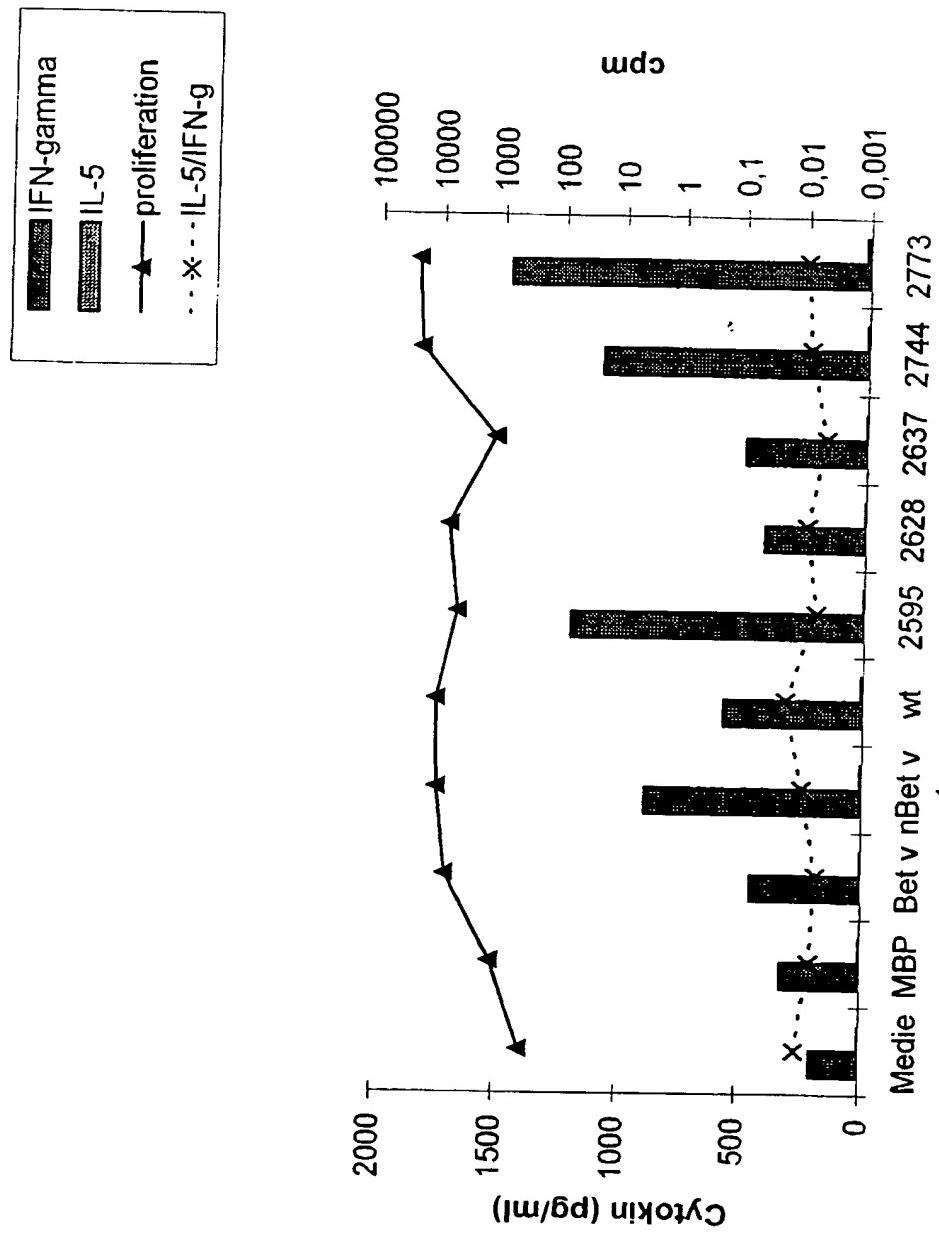


FIG. 42

Y O S A Y A M I S H I T O G U



1
Allergen
FIG. 43

Medie DB 1938 1953 1963 1974 1981 1991

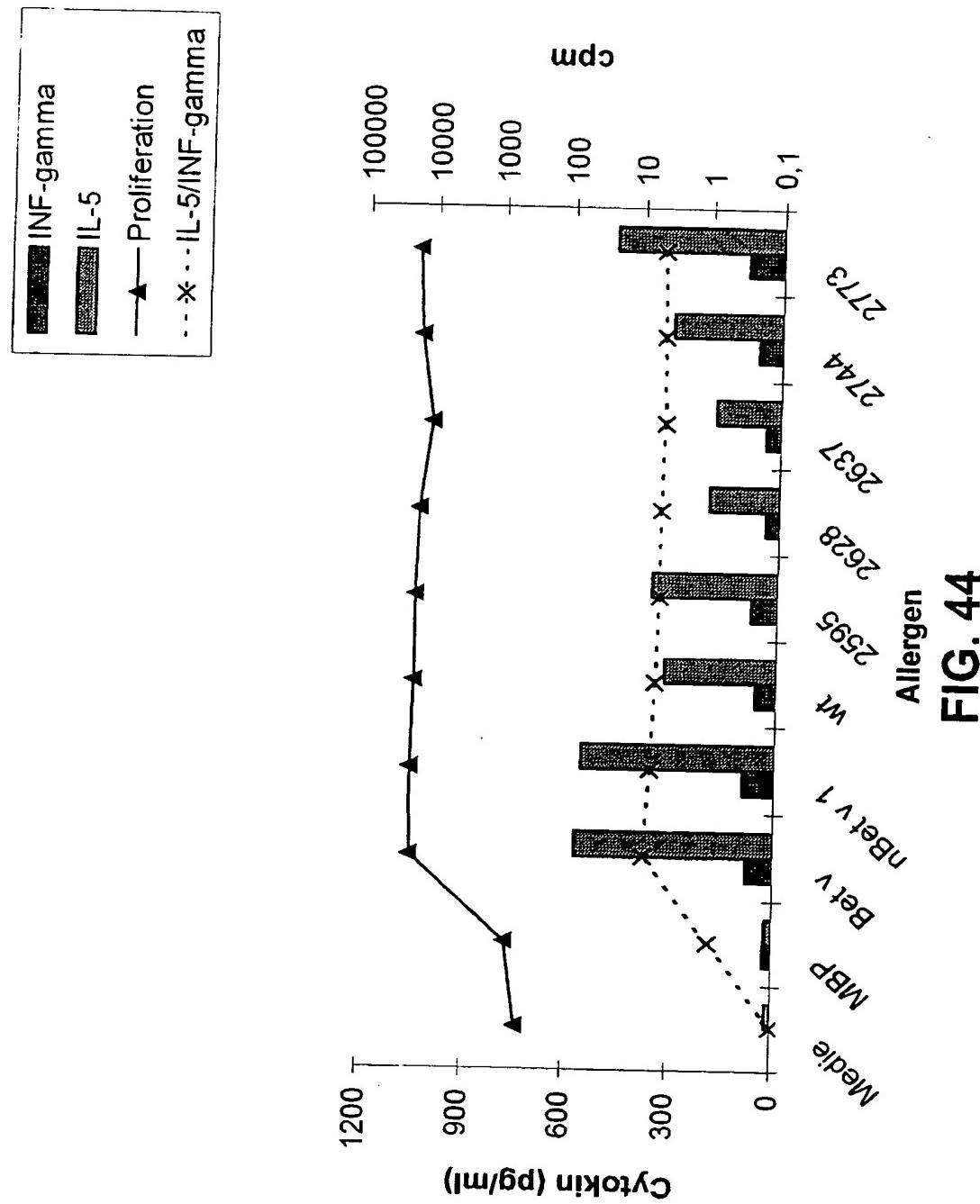


FIG. 44